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Sequence 299, Application US/09556877

Patent No. 6432916

GENERAL INFORMATION:

APPLICANT: Probst, Peter

APPLICANT: Bhatia, Ajay

APPLICANT: Skeiky, Yasir

APPLICANT: Hing, Steve

APPLICANT: Maisonneuve, Jeff

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

FILE REFERENCE: 210121.469C5

CURRENT APPLICATION NUMBER: US/09/556,877

CURRENT FILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 305

SOFTMARE: FastSEQ for Windows Version 3.0/4.0
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; TYPE: PRT
; ORGANISM: Chlamydia
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US-08-460-209-4
US-08-125-077-4
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US-09-541-782-6
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US-09-373-155-33
US-09-369-974-33
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Pred. No. 9e-109;
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Sequence 4318, Appli
Sequence 4, Appli
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US-09-620-412C-299
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                             GENERAL INFORMATION:

APPLICANT: LYNN DOUCETTE-Stamm et al
APPLICANT: LYNN DOUCETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
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LENGTH: 361
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
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APPLICATION NUMBER: US 60/055,779 FILING DATE: 1997-08-14
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US-09-134-001C-4463 Sequence 4463, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNO FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13

AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS

TO STAPHYLOCOCC

PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08

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; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3159
; LENGTH: 10182
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159
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                                                                                                                                                                                         INEDSDKQKT----YNDKIQAAKEIINQTSNPTLDK-----
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Pred. No. 1.0
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RESULT 5
US-09-308-375-2
(Sequence 2, Application US/09308375
; Sequence 2, Application US/09308375
; Patent No. 6300117
; GENERAL INFORMATION:
APPLICATT: Genencor International, Inc.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394-PCT
CURRENT APPLICATION NUMBER: US/09/308,375
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: EP9719636.4
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; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4463
; LENCTH: 2137
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4463
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LENGTH: 2285
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows V
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                              L-EREFVDGERSLAESQENAFRKQPAFIQQVLVNIASLFSGY 658
                                                               GAFAALGWALESLISSFAEAKKAKDD-----FEQSQQTNVEAITTNKDSTDKLIQQ
                                                                                               DVYSRL-QVLDSLMSTIVSNPQANQEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQ
                                                                                                                                               SLFYGAISGLKEMVSQAIEIDTLMTN-----IRRVMNEPDYKYNELLQESIDLGDT-L
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YKELQKVKESRSLTSDEEQEYLQ----VTQQLAQTFPALVKGY
                                                                                                                               TLLLSKNTRTLASSLILGTRAMGQETLATAGLEAGMTRAAVASRVLKTALRGLLVSTLVG
                                                                                                                                                                                              NKLQNNFTEFAIAASDAF---ISDGLIEFTQAAGSLLNASTGVIKSVGFLPPLLAAVSTA
                                                                                                                                                                                                                        KQLYK--TAFSSTSSSSYAAALSDGYSAY-KTLNSLYSESRSGVQS------AISQTA 520
                                                                                                                                                                                                                                                             SDAQKQNTSIGVAGIYQLSRFNAMMNNFSIAQNAAKTAANSTGSAWSEQQKYADSLQARV
                                                                                                                                                                                                                                                                                            AQALKQPSADGLA-----TAM---GQVAFAAAKVGGGSAGT-----AGTVQMNV
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RESULT 6 US-09-134-001C-5080 ; Sequence 5080, App

5080, Application US/09134001C

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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14
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Best Local (
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SEQ ID NO 5080
LENGTH: 3696
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TYPE: PRT
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QAQTNQQ--VSDAKTEAID---TITNIQANVAKKPSARVE 1714
                                          NSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAFIQ 645
                                                                                                                                                                           QOINQIQTHQTATTEEKEAAIQLANQKSNEA-----RTAIQNEHSNNGVAQAKSNGTHE 1620
                                                                                                                                                                                                                                                                                                                 ALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALS 492
                                                                                                                                                                                                                                                                                                                                                            SRINAQ----VVEKESARN-----AIEQKATQQT-QFINNNDNATDEEKEVANNLVI 1514
                                                                                                                                                                                                                                                                                                                                                                                          AAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQ 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEQINH----IQNTPDATNEEKQEAINRVSAELARVQAQINAEHTTQGVKTIKDDAITSL 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K---IEAKDNIQRNSTRDQVNEAKTNGINKIENITPATTVKSEARQ-----AVQNKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTRLTQAKET-----ALNDINQAQTNQNVDTALTSGIQNIQNTQVNVRKKQEAKTTIND 1255
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                                                                                                                                                                                                                        DGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQRAAETIVR 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKA 312
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                                                                                  IELVMPDAHKKSDAKQSIDNKYNEQSNTINTTPDATDEE-KQKALDKLKIAKDAGYNKVD
                                                                                                                   DSQTLGDVYSRLQVLDSL------MSTIVSNPQANQEEIMQKLTASISKAPQFGYPAVQ 605
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RESULT 7

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. Db 275 AI	ОУ 206 ОТЕ	217	Ov 158	Db 160 ARI	100	Qy 59 LS:	Db 40 ETS	Оу 13 ЕS	Query Match Best Local : Matches 15	US-08-687-956A-2	2	FRAGM	TOGYH					H	н			AT							8)			STREET:		ΩZ	; TITLE O	APPLIC	APPLIC		US-08-687-956A-:
AIQ-QRNAQAKADYEAKLAQYEKDLAAAQSGNATNEADYQAKKAAYEQEL 323	OQIIKDLERQNISYEAVLTNAGEVIK	QQANNDSQAAYAAAKEAYDKELARVQAANAAKKEYEEALAANTTKNEQIKAENA 27	NNIKKALEAOKDTIDKLNKLYTLONONKSLTEVL-KTTDSADOIPAINS 205	ARNOW DIANSULDMAN LABELE INWALLEMANLY DEKKANSUFSNIM I EDV	TEDYKAAV 15	LSSAKNALISLRDAILNKNSSPT-DSLSQLEASTSTSTVTRVAAKDYDE 106	G	ESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSF 58	h 6.1%; Score 194.5; DB 2; Length 1566; Similarity 21.0%; Pred. No. 5.8e-05; 57; Conservative 116; Mismatches 281; Indels 195; Gaps	Streptococcus sobrino	SOURCE:	ENT TYPE: internal	ITCAL: NO	TYPE	DEDNESS: single	amino acid	H: 1566 amino acids	INFORMATION FOR SEQ ID NO: 23:	ION:	REFERENCE/DOCKET NUMBER: 50885/222892	S, PAUL N	Y/AGENT INFORMATION:	APPLICATION NUMBER: GB 9401689.6	G DATE: 29-UOL-1996 IFICATION: 536	APPLICATION NUMBER: US/08/687,956A	APPLICATION DATA:	DOS	TER: IBM PC compatible	READAB	20005	RY: USA	WASHINGTON	FLOOR	PILLSBURY, MADISON & SUTRO, LLP	ORRESPONDENCE ADDRESS:	INVENTION: INFECTIONS DUE TO STREPTO	TOVENTION:	2	51157	6A-23 3. Application US/08687956A

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                           APPLICATION NUMBER: US/07/6
FILING DATE: APTI1 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A
REGISTRATION NUMBER: 29,775
                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION UNBER: PCT/US93/03077 FILING DATE: 19930331
                                                                        REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1540
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL TITLE OF INVENTION: REGULATING GENE EXPRESSION NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Board of Regents, The Universityof Texas APPLICANT: Gaynor, Richard B. APPLICANT: Wu, Foon Kin
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. I
                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 77210
                                       TELEX
                                                      TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVLQAQQNNSPDNIAATKELID---AAETKVN-ELKQEHTGLTDSPLVKKA--EEQISQA 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFTFYDEDGN-----PIDFDNALLSVASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Arnold White & Durkee P.O. Box 4433
                                                        713-749-2679
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US-08-353-700-1

Sequence 1, Application US/08353700
Patent No. 5599919
GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTNER, JEROME B.
TITLE OF INVENTION: MUCLEIC ACID ENCODING APPLICANT: TRANSIENTLY-EXPRESSED

A KINETOCHORE PROTEIN,

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; LENGTH: 1093 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-03077-1
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Best Local Similarity 19.2%;
Matches 145; Conservative 14
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RAATEELLANKIQMSSMESQNSLLRQENSRFQAQL
                                                                                                               MSTI-----VSNPQA---NQEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLERE 621
                                                                                                                                                                                         IESQ-----GRSADASQRAAETIVRDSQTL----GDVYSRLQ-----VLDSL 570
                                                                                                                                                                                                                                                                                                                                                                                       ADLLKEKDEQIRGLMEEGEKLSKQQ--LHNSNIIKKLRAKDKENENMVAKLNKKVKELEE 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKKAEEQI------SQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YETKMADLMAA------LQDMERLANSDPSNNHTEEVNNIK-KALEAQKDTIDKLNKLV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKEQKHEDRQSNTPSPPVSTFSSGTSTTSDIEVLDHESVISESSASSRQETTDSKSSLHL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDE--AKSNFDTAKSGLENAKTLAE 126
                                      FVDGERSLA-----
                                                                                                                                                       EEARQQQETLAIQVGDLRLALQRTEQAAARKEDYLRHEIGELQQRLQEAENRNQELSQSV
                                                                                                                                                                                                                                  --EEKNRSIQAALD---SAYKELTDLHKANAAKDSEAQEAALSREMKAKEELSAALEKAQ 704
                                                                                                                                                                                                                                                                      FSSTSSSSYAAALSDGYSAYKTLNSLY----SESRSGVQSAISQ--TANPALSRSVSRSG
                                                                                                                                                                                                                                                                                                                                                 EIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGG---GSAGTAGTVQMNVKQLYKTA 478
                                                                                                                                                                                                                                                                                                                                                                                                                           SLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAEAEKKVQLACKERDAAKKEIKNIKEE-------------------------LATRLNSSET 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKLEKREAQLLSLSKEKALLEEAFDNLKDEMFRVKE----ESSSISSLKDEFT-----QR 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELSGKGYALVPIIVNSSTPKSKTVESAEGKSEEVNETLVIPTEEAEMEESGRSATPV--N 404
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                                                                                                                                                                                                                                                                                                            ELQHLKQVL-----DGKEEVEKQHRENIKKLNSMVERQEKDLGRLQVDMDEL----
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                                                                            SSTTRPLLRQIENLQATLGSQTSSWEKLEKNLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------AVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPL 308
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                                  ESQENAFRKOPAFIQQVL
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Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                              1060
                                                                                                                                                                                                                          1180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1000 FANYIDEREKSISELSDQYKQEKLILLQRCEETGNAYEDLSQKYKAAQEKNSKLECLLNE 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: AND NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: REED, JANET E. REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 ESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRDA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
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KILNDDSGLLHGELVEDIPGGEFGEQPNEQHPVSLAPLDESNSYEHLTLSDKEVQMHFAE
                                                                         QCSLQTTMNKLNELEKICEILQAEKYELVTELNDSRSECITATRKMAEEVG---KLLNEV
                                                                                                                                               HELQTIRGDLETSNLQDMQSQE-----ISGLKDCEIDAEEKYISGPHELSTSQNDNAHL 1289
                                                                                                                                                                                    QALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKEL-IDAAE--------
                                                                                                                                                                                                                                                                                                                                   NHTEEVNNIKKALEAQKDTIDKLNKLVT-LQNQNKSLTEVLKTTDSADQI---PAINS-- 205
                                                                                                                                                                                                                                                                                                                                                                                                             AKSNFDTAKSGLEN-----AKTLAEYETKMA------DLMAALQDMERLANS---DPSN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILNKNSSPTDSLSQ------LEASTSTSTVTRVAAKDY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETLSLEKKEMSSIIS----LNKREIEELTQENGTLKEINAS-----LNQEKMNLIQKSES
                                  KPSGSDIPIVG------PSGSAASAGS-----AAGALKSSNNSGRISLLLDDVDNEMAA 374
                                                                                                                                                                                                                         ERESERNQCNFKPQMDLEVKEISLD----SYNAQLVQLEAMLRNKELKLQESEKEKECLQ
                                                                                                                                                                                                                                                                                                  NSKSEAGGIKQEIMTLKEEQNKMQKEVNDLLQENEQLMKVMKTKHECQNLESEPIRNSVK 1179
                                                                                                                                                                                                                                                                                                                                                                          CTSLCENRKNELEQLKEAFAKEHQEFLTKLAFAEERNQNLMLELETVQQALRSEMTDNQN 1119
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                                                                                                            ----TKVNELK-----QEHTGLTDS----PLVKKAEEQISQAQKDIQEI 326
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                                                                                                                                                                                                                                                             ----QLEINKNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIKLG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 189.5; DB 1
Pred. No. 0.00036;
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Matches 164;

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                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                    TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yen, Timothy J.

APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and I
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                                                                                                         ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Philadelphia
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                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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Score 189.5; DB 5;
Pred. No. 0.00036;
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US-09-336-447A-76

; Sequence 76, Application US/09336447A

; Patent No. 6310190
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                                                                                                                                                                                    GENERAL INFORMATION:
                               APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS
FILE REFERENCE: AMCY:024
                                                                                                      APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
CURRENT APPLICATION NUMBER: US/09/336,447A CURRENT FILING DATE: 1999-06-21
                                                                                                                                                               APPLICANT: HANSEN, ERIC J.
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                                                    OF MORAXELLA CATARRHALIS
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LENGTH: 3788

TYPE: PRT
OGGANISM: MORAXELLA CATARY
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1036)..(3786)
OTHER INFORMATION: Xaa - a
US-09-336-447A-76
RESULT 12
US-08-428-414A-3
; Sequence 3, Application
; Patent No. 5912166
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                                                                                                                      QIDNPRTEINLINEARNA
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                                                                                                                                                                                                                                                                                                                      SGVQSA-ISQTANPALSRSVSRSGIESQGRSADASQRAAETIVRDSQTLGDVYSRLQVLD 568
                                                                                                                                                                                                                                                                                                                                                                NAEEGLLDLSGRSEQIDNPRTEINLINEARNALSGRLIDQKASEQIDNPRTEINLINEAR
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TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND
TITLE OF INVENTION: LEISHMANIASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
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657
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REGISTRATION NUMBER: 39,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/428,414A FILING DATE: 21-APR-1995 CLASSIFICATION: 436
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                                                                                                                                                                                                             RLKEEQARKERELLKEMAKK----DAALSKVRRRLDA-----EIASEREKLE 546
                                                                                                                                                                                                                                                                                                      NSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAINS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWSFLSSAKNALISLRDAILNKNS-----SPT-----DSLSQLEASTSTSTVTRVA- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGSERVAQSQ-----VEGQ-----QFKEATHINLSLTTLGRVIDVLADMATKGAKAQYS 340
                               ISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEA-----QLTAMS
                                                                                                                                       STVAQLEREQREREVA-----LDALQTHQRKLQEALESSERTAAERDQLLQQLTELQSER
                                                                                                                                                                        AAVLQAQQNNSPDNIAATKELIDAAETKVNELKQ-----EHTGLTDSPLVKKAEE-----
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                                                                                                                                                                                                                                                                                  ----EREHNQVQERLLRATEAEKSELE--SRAAALQE-----EMTATRRQADKMQALNL 503
                                                                                                                                                                                                                                                                                                                                                      VNEDPRARRIRELEEQMEDMRQAMAGGDPAYVSELKKKLALLESEAQKRAADLQALER--
LELATEWED-----ALRE-RALAER----DEAAAAELDAAASTSQNARESACERLTSLE
                                                                    TQLSQVVTDRERLTRDLQRIQYEYGETELARDVALCAAQEMEARYHAAVFHLQT-----L
                                                                                                     -QISQA-----QKDIQEIK-----PSGSDIPIVGPSGSAASAGSAAGALKSSNNSGR 360
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.00017;
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                                                                 Query Match
Best Local S
                                                  Best Local Similarity
Matches 116; Conserv
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                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: POLYPEPTIDE I
TITLE OF INVENTION: OF COMPETITI
TITLE OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1561 amino acids
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/GB96/00207
FILING DATE: 31-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                 TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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CLASSIFICATION: 536
ADDITE: 31-JUL-1997
ADDITE: 35/08/894,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2000 Peni
CITY: Washington
TOPOLOGY:
                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                   TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                     NAME: Murashige, Kate REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                  LENGTH:
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6024958
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19.4%;
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OF COMPETITION WITH STREPTOCOCCUS MUTANS ANTIGEN I/II
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                                                                                                                                                                                                                                                                                                                                     29,959
                                                  110;
                                                Score 183.5; DB 3;
Pred. No. 0.00033;
10; Mismatches 270;
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                                                                                   Length
                                                  Indels
                                                                                   1561;
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                                                  Gaps
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RESULT 14
US-08-466-390-4
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   TELEFAX: (617)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: PITCHER ESO, EDMIND
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MAI
TITLE OF INVENTION: INTERIOR
                                                                                                                                                                                                SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVK
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Sequence 4, Application US/0847
Patent No. 5698439
GENERAL INFORMATION:
APPLICANT: TOUKATLY, GARY
APPLICANT: LIDGARD, GRAHAM
TITLE OF INVENTION: NOVEL &
TITLE OF INVENTION: INTERIO
                                                                                                                           RESULT 15
US-08-470-950-4
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-390-4
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Best Local Similarity
1017
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LENGTH: 2101 amino aci
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                                                                                                                                     DASQRAAETIVRDSQTLGDVYSRLQVLDSLMST--IVSNPQANQEEIMQKLTASISKAPQ 598
                                                                                          CSTQAALQAMEREAEQMGNELERLRA--ALMESQGQQQEERGQQEREVARLTQERGRA--
                                                                                                                                                                                     MAATSKEVARLETL----VRKAGEQ---QETASRELVKEPARAGDRQPEWLEEQQGRQF
                                                                                                                                                                                                                                        AAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSG-----IESQGRSA 540
                                                                                                                                                                                                                                                                                       LQEAKEKVAGIESHSELQISRQQNKLAELHANLARALQQVQEKEVRAQKLADDLSTLQEK 908
                                                                                                                                                                                                                                                                                                                                       VAFAAAKVGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                  QLTAMS--DQLVGADGELPAEIQAIKDALAQALKQPSADG-----LAT-----AMGQ 448
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                                          FGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQP---AFIQQVLVN 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKAETRSLVEQHKRERKELEEERA--GRKGLEARLLQLGEAHQAETEVLRRELAEAMAA
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-----QADLALEKAARAELEM------RLQNALNEQRVEFATLQEALAH
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Conservative 121;
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Pred. No. 0.00051;
Pred. No. 0.2025;
                                                                                                                                                                                                                                                                                                                                     ----GSAGTAGTVQMNVKQLYKTAFSSTSSSSY
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GRAHAM P
NOVEL MALIGNANT CELL TYPE
INTERIOR NUCLEAR MATRIX

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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HU
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LENGTH: 2101 amino aci
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REFERENCE/DOCKET NUMBER: MT
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 536
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                                      QHTAESECEQLV-----KEVAAWRDGYEDSQQEEAQYGAMFQEQLMTLKEECEKARQE
                                                                        QLTAMS--DQLVGADGELPAEIQAIKDALAQALKQPSADG-----LAT-----AMGQ 448
                                                                                                                                                                                                                                                                                               AGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQIS- 317
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                                                                                                               ELKAETRSLVEQHKRERKELEEERA--GRKGLEARLLQLGEAHQAETEVLRRELAEAMAA
                                                                                                                                               NNSGRISLLLD------DVDNEMAAIALQGFRSMIEQFNVNNPATAKEL-----QAMEA 403
                                                                                                                                                                                    ------QAQKDIQEIKPSGSDIPIVGPSGSAASAGS------AAGALKS----S
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617) 248-7100
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Best Local Similarity
Matches 161; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTT
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: TESTA, HU
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450 LLAERGHFEEEKQQLSSLITDLQSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTT 509
                          123 TLAE---YETKMADLMAALQDME-RLANSDPSNHHTEEVNNIKKA-LEAQ----KDTIDK 173
                                                                       396 QLQDNPPQEKGEVLGDVLQLETLKQEAATLAANNTQL-----
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                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
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CLASSIFICATION: 424
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SYSTEM: PC-DOS/MS-DOS
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US-08-195-487-4
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APPLICANT: TOUKACTLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/195,487
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1017
                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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ZIP: 02109
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
 1017
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                          541 DASQRAAETIVRDSQTLGDVYSRLQVLDSLMST--IVSNPQANQEEIMQKLTASISKAPQ 598
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                                                                     CSTQAALQAMEREAEQMGNELERLRA--ALMESQGQQQEERGQQEREVARLTQERGRA--
                                                                                                                                               MAATSKEVARLETL----VRKAGEQ---QETASRELVKEPARAGDRQPEWLEEQQGRQF
                                                                                                                                                                                 AAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSG-----IESQGRSA 540
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                                FGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQP---AFIQQVLVN 650
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-QADLALEKAARAELEM------RLQNALNEQRVEFATLQEALAH
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RESULT 18 US-08-483-924-4 ; Sequence 4, Application ; Patent No. 5882876

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REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LIGGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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CITY: BOSTO
STATE: MA
COUNTRY: US
ZIP: 02110
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/483,924 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDALNELTEEHSKATQEWLEKQAQLE--KELSAALQDKKCLEEKNEILQGKLSQLEEHLS 395
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ELKAETRSLVEQHKRERKELEEERA - - GRKGLEARLLQLGEAHQAETEVLRRELAEAMAA
                                                                                                                                         ARDSAQTSVTQAQREKA-ELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQQKAT
                                                                                                                                                                                                                VAEKQEATRODHAQQLATAAEEREASLRERDAALKQLEALEKEKAAKLEILQQQLQVANE
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                                 NNSGRISLLLD-----QAMEA 403
                                                                   EKERVAQEKDQLQEQLQALKES
                                                                                                                                                                            AGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQIS-
                                                                                                                                                                                                                                                      IIKDLERQNISYEAVLTNAGEVIKAS---SEAGIK------LGQALQSIVD
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125 HIGH STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%; Score 183.5; DB 2; 20.8%; Pred. No. 0.00051;
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                                                                     -LKVTKGSLEEEKRRAADALEEQQRCIS
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PRIOR APPLICATION NUMBER: 60/11/
PRIOR FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2101
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bissell, Mina
TITLE OF INVENTION: UTILIZATION OF NUCLEAR STRUCTURAL PROTEINS
TITLE OF INVENTION: THERAPH AND DETECTION OF PROLIFERATIVE AND
TITLE OF INVENTION: DIFFERENTIATION DISORDERS
FILE REFERENCE: IB-1454- Sequence Submittal
Patent No. 6.887790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09452294 Patent No. 6287790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                 TLAE---YETKMADLMAALQDME-RLANSDPSNNHTEEVNNIKKA-LEAQ----KDTIDK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIASNSETKESTKASEASPSASSSVSSWSFLSSA---KNALISLRDAILNKNSSPTDSLS
                                                                            VAEKQEATRQDHAQQLATAAEEREASLRERDAALKQLEALEKEKAAKLEILQQQLQVANE
                                                                                                                                                                                                     LNKLYTLQNQ------NKSLTEVLKTTDSAD-----QIPAINSQLEINKNSADQ
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ARDSAQTSVTQAQREKA-ELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQQKAT
                                    AGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQIS-
                                                                                                                  IIKDLERQNISYEAVLTNAGEVIKAS---SEAGIK------LGQALQSIVD
                                                                                                                                                          LNATIQQQDQELAGLKQQAKEKQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQKEQQLKE
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PCT-US93-06160-4
                                       Query Match
Best Local Similarity
Matches 161; Conserv
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                                                                                                                                                                                                   TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:

NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-
TELECOMMUNICATION INFORMATION:
TELECHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US93/06160
FILING DATE: 19930671
CLASSITETO.
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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29 QIASNSETKESTKASEASPSASSSVSSWSFLSSA---KNALISLRDAILNKNSSPTDSLS 85
                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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53 STATE STREET
                                         Conservative 121; Mismatches 282;
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                                                            5.7%; Score 183.5; DB 5; 20.8%; Pred. No. 0.00051;
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                                                                               Length 2101;
                                       Indels 211; Gaps
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	QADLALEKAARAELEMRLQNALNEQRVEFATLQEALAH 1054	1017	Db
	FGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAFIQQVLVN 650	599	Qy
1016	CSTQAALQAMEREAEQMGNELERLRAALMESQGQQQEERGQQEREVARLTQERGRA	961	Дb
598		541	Qy
960	MAATSKEVARLETLVRKAGEQQETASRELVKEPARAGDRQPEWLEEQQGRQF	909	ДĎ
540	AAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSA	488	Qy
806	LQEAKEKVAGIESHSELQISRQQNKLAELHANLARALQQVQEKEVRAQKLADDLSTLQEK	849	дь
487		449	Qy
848	QHTAESECEQLVKEVAAWRDGYEDSQQEEAQYGAMFQEQLMTLKEECEKARQE	796	рь
448	QLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQ	404	Qy
795	ELKAETRSLVEQHKRERKELEEERAGRKGLEARLLQLGEAHQAETEVLRRELAEAMAA	738	Db
403	NNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEA	356	Qy
737	EKERVAQEKDQLQEQLQALKESLKVTKGSLEEEKRRAADALEEQQRCIS	689	DЪ
355	QAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSS	318	γo
889	ARDSAQTSVTQAQREKA-ELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQQKAT	630	ДĎ
317	AGDOSQAAVLQAQQUNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQIS-	259	Qγ
629	VAEKQEATRQDHAQQLATAAEEREASLRERDAALKQLEALEKEKAAKLEILQQQLQVANE	570	Дb
258	IIKDLERQNISYEAVLTNAGEVIKASSEAGIKLGQALQSIVD	217	Qy
569	LNATIQQQDQELAGLKQQAKEKQAQLAQTLQQQEQASQGLRHQVEQLSSSLKQKEQQLKE	.510	Db
216	LNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQ	174	Qy
509	LLAERGHFEEEKQQLSSLITDLQSSISNLSQAKEELEQASQAHGARLTAQVASLTSELTT	450	дд
173	TLAEYETKMADLMAALQDME-RLANSDPSNNHTEEVNNIKKA-LEAQKDTIDK	123	Qy
449	QLQDNPPQEKGEVLGDVLQLETLKQEAATLAANNTQLQARVEMLETERGQQEAK	396	рь
122	QLEASTSTSTYTRVAAKDYDEAKSNFDTAKSGLENAK	86	Qy
395	ODALNELTEEHSKATQEWLEKQAQLEKELSAALQDKKCLEEKNEILQGKLSQLEEHLS	338	DЪ

RESULT 21
US-08-006-676B-1
Sequence 1, Application US/08006676B
Patent No. 5411865
; GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey B. Oster
STREET: 8339 SE 57th Street
CITY: Mercer Island
STATE: Washington
COUNTRY: USA
ITP: 98040-4906
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD for Windows
CURRENT APPLICATION DATA:

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Best Local !
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REFERENCE/DOCKET NUMBER: REI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 232 7845
TELEPHONE: (206) 236 0205
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/006,676B FILING DATE: 15-JAN-1993 CLASSIFICATION: 435
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TRAALEQQLRDSEERA 949
                                                                     QLESTTAAKMSAEQDRESTRATLEQQLRDSEERAAEL - - - ASQLEATAAAKSSAEQDREN
                                                                                                     SLMSTIVSNPQANQEE-----IMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREF 622
                                                                                                                                         ASQLESTTAAKMSAEQDRESTRATLEQQLR--ESEERAAE-----
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                                 VDG--ERSLAESQENA 636
                                                                                                                                                                       -SGVQSAISQTANPALSRSVSRSGIESQGRSADASQRAAETIVRDSQTLGDVYSRLQVLD 568
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RESULT 22
US-08-282-845-2
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CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1005/587-0430
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: A 230Kd Antigen Present in
TITLE OF INVENTION: Species
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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VALDALQTHQRKLQEALESSERTAAER---DQLLQQLTELQSERTQL--SQVVTDRE---
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                                                                                                                                                                                                                                                                                                                                            AGSERVAQSQ-----VEGQ-----QFKEATHINLSLTTLGRVIDVLADMATKGAKAQYS 340
                                AAV--LQAQQN-----NSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQI 316
                                                                   RLKEEQARKERELLKEMAKKDAALSKVRRRKDAEIASERE---KLESTVAQLEREQRERE
                                                                                                 QL-EINKNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQ
                                                                                                                                     ----EREHNQVQERLLRATEAEKSELE--SRAAALQE-----EMTATRRQADKMQALNL
                                                                                                                                                                       NSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAINS 205
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; TOPOLOGY: 1:
; MOLECULE TYPE:
PCT-US94-00324-1
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PCT-US94-00324-1
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GENERAL INFORMATION:
APPLICANT: Reed, Steven
Query Match
Best Local Similarity
                                                                                                                                               TELEFAX: (206) 233-06.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                              NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 500-TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
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APPLICATION NUMBER:
FILING DATE: 15-JAN-
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NUMBER OF SEQUENCES:
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OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word, version 5.1a
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                   Sequence 5, Application Patent No. 6310190
                                                                                     APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS
FILE REFERENCE: AMCY:024
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CURRENT APPLICATION NUMBER: US/09/336,447A CURRENT FILING DATE: 1999-06-21 NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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TYPE: PRT
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                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                        APPLICANT: Zhu, Xuellang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
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                                                                                   STREET:
CITY: S
STATE:
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                                                    ZIP:
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COMPUTER:
                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 HMESGPESVSSNQSSMNPII------NGQIASNSETKE----STKASEASPSASS 51
                                                                                                                                                                                                                                                                                                                                                                    ERQTAGGIANAIAIATLPSPSRAGEHHVLFGSGYHNGQAAVSLGAAGLSDTGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVAFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETKVNELKQEHTGL------TDSPLVKKAEEQISQAQKDIQEIKPS----GSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLLDQKADIDNNINNIYDLAQQQDQHSSDIKTLKKNVE--EGLLDLSGRLI----DQKADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKTAIER-----NFNRTVVNGFEIEKNKAGIAKNQADIQTLENNVGEELLNLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVS-----SWSFLSSAKNALI---SLRDAILNKNSSPTDSLSQLEAST
                                                                                                                                                                                                                                                                                                                                                                                                       YSESRSGVQSAISQTANPALSR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KTLAKVSAANTDRIAKNKAEADASFETLTKNQNTLIEQG-EALVEQ----NKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKDIKTLENNVEEGLLDLSGRL--IDQKADIAKNQADIAQNQTDIQDLAAYNELQDQYAQ
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                                                  92122
                                                                                     San Diego
: California
                                                                    USA
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IBM PC
              Floppy disk
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compatible
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-0CT-1993
ATTORNEY_AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                    604 HELQTIRGDLETSNLQDMQSQE-----ISGLKDCEIDAEEKYISGPHELSTSQNDNAHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 ESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRDA 72
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GIESQGRSADASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQANQEEIMQKLTA 591
                                      VFCSSLQEENLTRKETPSAPAKGVEELESLCEVYRQSLEKLEEK---
                                                                           LYKTAF--SSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRS
                                                                                                                  GLEEGLYPSLSSSCYPDSSSL-SSLGDSSFYRALLEQTGDMSLLSNLEGAVSANQCSVDE
                                                                                                                                                                                                                                                                            KILNDDSGLLHGELVEDIPGGEFGEQPNEQHPVSLAPLDESNSYEHLTLSDKEVQMHFAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKEL-IDAAE--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKSNFDTAKSGLEN-----AKTLAEYETKMA-------DLMAALQDMERLANS----DPSN 151
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                                                                                                                                                         AIKDALAQALKQ---PSADGLATAMGQVAFAAA---KVGGGS----AGTAGTVQMNVKQ
                                                                                                                                                                                                  LQEKFLSLQSEHKILHDQHCQMSSKMSELQTYVDSLKAENLVLSTNLRNFQGDLVKEMQL 834
                                                                                                                                                                                                                                       ----IALQGFRSMIEQFNVNNPATAKELQ----AMEAQLTAMSDQLVGADGELPAEIQ- 424
                                                                                                                                                                                                                                                                                                                 KPSGSDIPIVG-----PSGSAASAGS-----AAGALKSSNNSGRISLLLDDVDNEMAA 374
                                                                                                                                                                                                                                                                                                                                                          QCSLQTTMNKLNELEKICEILQAEKYELVTELNDSRSECITATRKMAEEVG---KLLNEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
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; MOLECULE TYPE: protein US-08-685-871-2
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US-08-685-871-2
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 7-26253
ETILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184102
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160
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                           169
                                                                 495
                                                                                                                                                                                                                              384
                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                         / Match 5.6%; Score 178.5; DB 3; Local Similarity 19.8%; Pred. No. 0.0006; nes 141; Conservative 123; Mismatches 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/685,871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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  DTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLE----INKNSADQIIKD----
                                                                                                                                                                                                                          PKAFVGNQL---PFVGFTYYSNRRYLSSANPND---NRTSSNADKSLQESLQKTIYKLEE 437
                                                                                                                                            QLHNE-MQLKDEMEQ-KCRTSNIKLDKI-MKELDEEGNQRRNLESTVSQIEKEKMLLQHR 494
                                                                                                                                                                                                                                                                PESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTLEMESKLAAEKKQTEQLSLELEVARLQLQGLDLSSRSL 1023
                                                               INEYORKAEQENEKRRNVENEVSTLKDQLEDLKKVSQNSQLAN---EKLSQLQKQLEEAN 551
                                                                                                                                                                                    AILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDE----AKSNEDTAKSGLENAKTLAEY- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MESQGIMKNKEIQELEQLLS-----SERQELDCLRKQYLS----ENEQWQQKLTS
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3000 K Street, N.W., Suite 500
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Akihiro
                                                                                                   ETKMADLMAALQDMERLA-NSDPSNNHTEEVNNIKKALEAQK 168
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US-09-310-187A-1
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APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
TITLE OF INVENTION: Graft Rejection
FILE REFERENCE: UCSF-090
CURRENT APPLICATION NUMBER: US/09/310,187A
CURRENT FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 3
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                     y match 5.5%; Score 175; DB 4; Length 1939; Local Similarity 19.7%; Pred. No. 0.0017; les 130; Conservative 125. Minimum.
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KTTDSADQIPAINSQL-EINKN--SADQIIKDLERQNISYEAVLTNA------GEVIK 240
                                                                                                                                                                   KNSSPTDSLSQLEASTSTSTV----TRVAAKDYDEAKSNFDTAKSGLENAKTLAEYETKM 131
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US-09-268-347-36
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SEQ ID NO 36
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Patent No. 6335182
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
FILE REFERENCE: 1038-860
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CURRENT FILING DATE: 199-03-16
NUMBER OF SEO ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
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AKVSDTLTIGGNTPTGGTTATPKVNITSTADGLNFAKETADA----SGSKNVYLKGIATT
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                                                                                                                                                 KTENLTTSIDEDNPTD--NGKDDALKAGDTLTFKAGKNLKVKRDGKNITFDLAKNLEVKT
                                                                                                                                                                                                                  -MERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSLTEVL-----KT
                                                                                                                                                                                                                                                                                          TVGNNGTAVTKGGFETVKTGATDADRGKVTVKDATANDADKKVATVKDVATAINSAATFV
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19.3%; Pred. No. (
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                                                                    -PAIN-----SQLEINKNSADQIIKDLERQNISYEAVLTN 234
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Mismatches 30
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-938-105-3
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GENERAL INFORMATION:
GENERAL THFORMATION:
APPLICANT: Leinwand, Leslie A.
APPLICANT: Vikstrom, Karen L.
APPLICANT: Vikstrom, Karen L.
APPLICANT: VIKSTION: TRANSGENIC MODEL FOR HEART FAILURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3,
                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1133
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                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1188
                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1886 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                       TELEFAX: (303) 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1700
CITY: Denver
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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Query Match Best Local

Local Similarity

5.4%; Score 173.5; DB 4; 21.7%; Pred. No. 0.0021;

Length

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; LENGTH: 873
; TYPE: PRT
; ORGANISM: Moraxella
US-09-336-447A-13
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                                                                                                   CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09336447A Patent No. 6310190
 Query Match
                                                                                                                                                                                                                                                                      APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
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                                                                                                                                                                                  APPLICANT: FISKE, MICHAEL J.

APPLICANT: FREDENBURG, ROSS A.

TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT: University of Kentucky Research Fo
APPLICANT: Timoney, John
APPLICANT: Artiushin, Sergey
TITLE OF INVENTION: Compounds Encoding the Pro-
TITLE OF INVENTION: and Assays Therefor
FILE REFERENCE: 50229-212
CURRENT APPLICATION NUMBER: US/09/103,664A
CURRENT FILING DATE: 1998-06-23
NUMBER OF SEO ID NOS: 10
SOFTWARE: Patentin version 3.0
SEO ID NO 2
LENGTH: 534
TYPE: PRT
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Matches 94
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Matches 124; Conservative
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                                                                                   Local Similarity
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                                                                   5.4%; Score 172; DB 4; 22.0%; Pred. No. 0.00045; ive 80; Mismatches 166;
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Live 97; Mismatches 238;
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CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION:
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APPLICANT:
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Best Local
                                                                                                                                                                                                                                                                                                                   Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FISKE, MICHAEL J.

APPLICANT: FREDENBURG, ROSS A.

TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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 RQNISYEAVLTNAGEVIK-----ASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPD
                                                                  DK----LNKLYTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQ----IIKDLE--
                                                                                                        DIAKNQADIAKNQADIQTL---
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21.6%; Pred. No. 0.0011;
ative 82; Mismatches 226;
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LENGTH: 676
TYPE: PRT
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Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4318, Application US/09134001C Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID, AND AUTITLE OF INVENTION: EPIDERMIDIS FOR D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14
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TTNQSDSDSKDDKSNDGRRSTLERIASDTDQIRDSKDQHVTDEKQDIQAITRSLQGSDKI
                                  ASAGSAAGALKSSNNSGRISLL--------LDDVDNEMAAI--ALQG----
                                                                    DDSEESVIDKLDKIQQDFKSDSNNKLSEQSDQQASPSNKNENNKEES------
                                                                                                     KELIDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSA 342
                                                                                                                                      KILSDLDSIAKNVDNRQQGENSA----SKPSDSTTDEKDDSNNKV---HDTNASTRNATT 188
                                                                                                                                                                       RQNISYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAAT 282
                                                                                                                                                                                                              ERLDKVDNQSSIDRIINDAKDKNNHLKSTDSS----ATSSKTEDDDTSEKDNDDMTKDLD
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                                                 TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 amino aci
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                             REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                       FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
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                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                   NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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Leivo, Ilmo
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Best Local Similarity
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                                     SGVQSAIS-QTANPALSRSVSRSGIESQGRSA--DASQRAAETIVRDS
                                                                           RPIRWYPNISTVMFKFRT-FSSSALLMYLATRDLRDFMSVELTDGHI-----KVSYDLG
                                                                                                                                                                                                                                                                                                           LFYLGSAKFIDFLAIEMR----KGKVSFLWDVGSGVGRVEYPDLTIDDS-----YWYRI 2233
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SGMASVVSNQNHNDGKWKSFTLSRIQKQANISIVDIDTNQEENIATSS
                                                                                                                                                     AVRVITFTGCMGETYFDNKPIGLWNFREKEGDCKGCTVSPQVEDSEGTIQFDGEGYALVS
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19.9%;
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Pred. No. 0.0069;
Prematches 259;
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RESULT 35
US-08-125-077-4
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Patent No. 5872231
Patent No. 5872231 5840863
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic Acids TITLE OF INVENTION: Fragments and
                                                                                                                                                      CITY:
                                                                                                                      COUNTRY:
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/919,95
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LA 97
TELECOMMUNICATION INFORMATION:
TELEPAN: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local 9
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PRIOR APPLICATION DATA: APPLICATION NUMBER: US PCT/US FILLING DATE: 21-SEP-1994
2407
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SGMASVVSNQNHNDGKWKSFTLSRIQKQANISIVDIDTNQEENIATSS
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                                  SGVQSAIS-QTANPALSRSVSRSGIESQGRSA--DASQRAAETIVRDS
                                                                       RPIRWYPNISTVMFKFRT-FSSSALLMYLATRDLRDFMSVELTDGHI-----KVSYDLG 2406
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TITLE OF INVENTION: METHOD FOR PREPARING VACCINE FOR DENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Patent No. 5352450
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Best Local :
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CURRENT APPLICATION DATA:
COURSENT APPLICATION DATA:
COURSENT APPLICATION DATA:
546 YDQ-KILQ
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                                   580 ANQEEIMQ
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FILING DATE: 29-MAY-1990
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mes 113; Conserv
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                                                                          HKNEDG--
                                                                                                                                                   ADAKADYEAKLAKYQADLAKYQKDLAD----YPVKLKAYEDEQTSIKAALAE-----LEK
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                                                                                                           SVSRSGIESQGRSADASQRAAETIVRD-----SQTLGDVYSRLQVLDSLMSTIVSNPQ 579
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RESULT 37 US-09-541-782-6

Sequence 6, Application Patent No. 6284480 GENERAL INFORMATION:

US/09541782

APPLICANT:

Nislow, Corey

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; TYPE: PRT
; ORGANISM: S.pombe
US-09-541-782-6
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APPLICANT:
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CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.
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APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal
FILE REFERENCE: 1015
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LDRLLQKV 909
                                   IQQVLVNI 651
                                                                                                       EIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAF 643
                                                                                                                                           NIGKIVSNFLQEQNESL; --YTKADILHSHLNDTNSNIRKANEIMNNRSEEFLRNAASQA
                                                                                                                                                                            DASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQ-------ANQE 583
                                                                                                                                                                                                                YNLQHTHEESQKELMYGVRNDIDALVKTCTTSLNDADIILSDYISDQKSKFESKQQDLIA
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                                                                   EIVGANKERIQKTVENG----SQLLDSKSKAIHSNSRSMYDHCLALAESQKQGVNLEVQT 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.2%; Score 167; DB 4; Length 1073; ilarity 17.7%; Pred. No. 0.0027; Conservative 123; Mismatches 284; Indels 19
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RESULT 38 US-09-723-820-6

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LENGTH: 1073
TYPE: PRT
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APPLICANT: Beraud, Christophe
TITLE OLVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/723,820
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
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 IQQVLVNI 651
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                                                                                                         NIGKIVSNFLQEQNESL---YTKADILHSHLNDTNSNIRKANEIMNNRSEEFLRNAASQA
                                                                                                                                          DASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQ----
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1995-06-12
EARLIER APPLICATION NUMBER: FR 95/07007
ARRLIER APPLICATION NUMBER: FR 95/07007
SARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1786
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 107; Conserv
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1078 GANSVNN----NKKLVNAEGLATALNNLSWTAKADKYADGESEGETDQEVKAGDKVTFKA 1133
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Search completed: March 12, 2003, 12:23:06 Job time: 77 secs

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ALIGNMENTS

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RESULT 1
AAU38921
ID AAU3
Chlamydia; sexually transmitted disease; PID; antibacterial; pelvic inflammatory disease; antigen; trachoma; gynecological; acute respiratory tract infection; atherosclerosis; male infertility; coronary heart disease.
        WPI; 2001-616771/71.
N-PSDB; AAS56995.
                                                                                                                                                                                                                                                     C. trachomatis CT875 protein.
                                       Bhatia A, Probst P,
                                                                                 21-APR-2000;
20-JUL-2000;
                                                                                                                                     01-NOV-2001
                                                                                                                                                                             Chlamydia trachomatis serovar E.
                                                                                                                                                                                                                                                                         16-JAN-2002 (first entry)
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                YPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAFIQQVLVNIASLFSGYLS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal. Methods from the present invention can be used: for detecting presence of Chlamydia in a patient; to stimulate and/or expand T cells specific for a Chlamydia protein; and for treatment of a Chlamydia infection. ABL92394 to ABL92709 and ABB94096 to ABB94374 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein and methods for the diagnosis and therapy of Chlamydia infection Chlamydia DNA and protein sequences from the present invention can have antibacterial and immunostimulant activities, and can be used in vaccines. Compounds from the present invention can be used for eliciting an immune response, specifically stimulating a Chlamydia-specific T-cell response or inhibiting the development of a Chlamydia infection in an immune compounds the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the development of a Chlamydia infection in an incomposition of the
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Chlamydia-specific T-cel
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93.9%;
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08-APR-1999;
01-OCT-1999;
22-OCT-1999;
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The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamdiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis
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                                                                                                                                                                                                                                                                                                              acid
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                                                                                                                                                                                                                                                                                                    polypeptide for diagnosis and treatment of Chlamydia infection
s immunogenic portion of Chlamydia antigen, which comprises
id sequence encoded by polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bhatia A,
                                                                                                                                                                                                                                                            Pages
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99US-0288594.
99US-0410568.
99US-0426571.
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     ed diseases and can
n tubal obstruction
C. trachomatis is
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     RRESULT 4
AAG83263
ID AAG8
XX AAG8
XX AAG8
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XX Prot
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X
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Best Local S
Matches 350
                                                       Probst P,
                                                                                                                                                                                03-DEC-1999;
19-APR-2000;
                                                                                                                                                                                                                                                            04-DEC-2000;
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                                                                                                      CORIXA
                                                    Bhatia A,
                                                                                                                                                      99US-0454684.
2000US-0556877.
2000US-0598419.
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                                                                                                         CORP.
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Skeiky

YAW,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the leading cause of preventable blindness worldwide. C. pneumonia major cause of acute respiratory tract infections in humans and is thought to play a role in the pathogenesis of atherosclerosis and coronary heart disease. The present sequence is a protein isolated present invention.
Chlamydia; vaccine; infection; fusion protein; antigen; pelvic inflammatory disease; trachoma; atheroslerosis; acute respiratory tract infection; Capl; CT529; OMCB; polymorphic membrane protein; pmp; thiol specific antiox
                                                              Protein encoded by
                                                                                                                                                                                                                                                        PAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 AA;
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                                                                                        (first
                                                               Chlamydia trachomatis
                                                                                                                                          Protein;
                                                                                       entry)
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97.0%;
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Pred.
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No. 3
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.9e-94;
                                                                clone
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                                                                CT622
  antioxidant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                           heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361;
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RESULT 5
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AC ABB9
XX Chla
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is provided in a specification relating to compounds and methods for the treatment and diagnosis of chlamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of chlamydia antigens and DNA sequences encoding such polypeptides. They are useful for vacchaating against chlamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia polypeptides and fusion proteins useful inflammatory disease, trachoma, acute respiratory atherosclerosis and heart disease -
                                                                                      Chlamydia sp.
                                                                                                                             Chlamydial infection; Chlamydia; vaccine; antigen; antibacterial; immunostimulant;
              20-JUL-2001; 2001WO-US23121.
                                      31-JAN-2002
                                                               WO200208267-A2
                                                                                                               Chlamydia-specific
                                                                                                                                                                                            05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis and heart
                                                                                                                                                                                                                                           ABB94234 standard; Protein;
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                                                                                                                                                                                                                                                                                                          s.
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                                                                                                                                                                                                                                                                                                          361
                                                                                                                                                                                                                                                                                                                                   660
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                                                                                                                                                                                         (first entry)
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                                                                                                                                                                 sequence SEQ
                                                                                                                 T-cell
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97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1690; DB 22
Pred. No. 3.9e-94;
4; Mismatches 7
                                                                                                                                                                 ID NO:299.
                                                                                                                                                                                                                                            A
                                                                                                                             immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                       detection; diagnosis;
                                                                                                                             response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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RESULT 6
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AC AAY3
AC OAY3
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AC OAY3
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AC OT-C
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DT O7-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sir
Matches 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccines. Compounds from the present invention can be used for eliciting an immune response, specifically stimulating a Chlamydla specific T-cell response or inhibiting the development of a Chlamydla infection in an animal. Methods from the present invention can be used: for detecting the presence of Chlamydla in a patient; to stimulate and/or expand T cells specific for a Chlamydia protein; and for treatment of a Chlamydia infection. ABI92394 to ABI92709 and ABB94096 to ABB94374 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes compositions comprising a Chlamydia protein and methods for the diagnosis and therapy of Chlamydia infec Chlamydia DNA and protein sequences from the present invention can lantibacterial and immunostimulant activities, and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel compositions comprising Chlamydia treatment of Chlamydia infection -
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23-APR-2001; 2001US-0841132.
                                                  07-OCT-1999
                                                                                                    AAY37572 standard;
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                                                                                                                                                                                       G
                                                                                                                                                                                                                                                                SSTSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRS
                                                                                                                                                                                                                                                                                                                                                                               PAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAF
                                                                                                                                                                                                                                                                                                                                                                                                                  RISLLLDDVDNEMAATAMQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                 RISLLLDDVDNEMAAIALQGERSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGEL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-179901/23
                                                                                                                                                                                                                                                                                                                  SSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRS
                                                                                                                                                                                                                                                                                                                                                                    PAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                 (first entry)
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Pred. No. 3.9e
4; Mismatches
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3.9e-94;
nes 7;
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the

Chlamydia trachomatis cellular envelope protein.

Vaccine;

eye disease;

conventional trachoma; nonendemic trachoma;

perihepatitis;

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RESULT 7
AAY37571
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Best Local
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28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 1227-1228; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of Chlamydia trachomatis
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               AAY37571
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                     QLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGT 463
                                                                                                                                    EIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAF 643
                                                                                                                                                                      LSRSVSRSGIESQGRSADASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQANQE
                                                                                                                                                                                                                      EIMQKLTASISKAPQFGYPAVQNSVDSLQKFAAQLEREFYDGERSLAESQENAFRKQPAF
                                                                                                                                                                                                                                                                       QLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGT
                                                                          IQQVLVNIASLFSGYLS
                                                                                                  IQQVLVNIASLFSGYLS
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trachomatis
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inclusion conjunctivitis; genital disease; perihepatitis;
uretritis; epidymitis; cervicitis; salpingitis;
; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0107077.
97FR-0015041.
97FR-0016034.
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              Protein;
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99.4%;
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: Pred. No. 9.4e
1; Mismatches
               350
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No. 9.4e-84;
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Best Local s
Matches 299
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28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                       of Chlamydia trachomatis (see AA201425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY36754 -Y37949 are encoded by open reading frames (ORFs) of the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nongonococcal ubartholinitis;
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       paratrachoma;
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              308
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                                                                                                                                                                                  SLRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAKSGLENAKTLAEY 127
LVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGS
                                                                                                                                                                                                                                              MESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALI
                                   TEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGI
                                                                                                                                   ETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSL 187
                                                                                                                                                                                                                                    MESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASSSASSSVSSWSFLSSAKNALI
                                                                                                                                                                                                                                                                                  al Similarity
299; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENSET
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                                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 1226-1227; 1755pp; English
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease; conventional trachoma; nonendemic trachoma; inclusion conjunctivitis; genital disease; perihepa uretritis; aplightis; cervicitis; salpingitis; pneumopathy; venereal lymphogranulomatosis.
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97FR-0015041.
97FR-0016034.
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; Pred. No. 8.9e
17; Mismatches
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                                                                                                                                                                                                                                                                                            1435; DB 20;
No. 8.9e-79;
                                                                                                                                                                                                                                                                                   16;
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Indels Length

2

Gaps 67

1;

89

246

186

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307

LVKKAEEQINQAQQDIQTITPSGLDIPIVGPSGS

340

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RESULT 8
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Best Local S
Matches 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is Chlamydia pneumoniae full-length 76 kDa protein. C. pneumoniae 76 kDa protein is used in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory in the diagnosis of the protein of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16a; Fig 1; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 kDa protein; bactericidal; diagnosis; prevention; treatment; pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases caused by C. pneumoniae.
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30-JUN-1999;
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174
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                                                                    LNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNI---SYEA
                                                                                                                                                                                     GPESVSSNQSSMNPIINGQIASNSETKESTKA-----SEASP--SASSSVSSWSFLSSAK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-687542/67.
DB; AAD02063.
TTELAKYASDNQAILDSLGKLTSFDLLQAALLQSVANNNKAAELLKEMQDNPVVPGKTPA
                                                                                                                                        TSLADIQAALVSLQDAVTNIKDTAATD-----EET----AIAAEWETKNADAVKVGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                   GPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAV 65
                                                                                                                                                                                                                                                                                       NALMSLADKLGTASSNSSSSTSRS-ADVDSTTATAPTPPPPTFDDYKTQAQTAYDTIFTS
                                                                                                                                                                                                                                                                                                                                     NALISLRD--AILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNEDTAKSGLENA
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33; Conservative
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for vaccinating against Chlamydia
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99US-0141276.
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Pred. No. 8.4e-46;
6; Mismatches 262
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a infections -
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                                                                                                                                                                                                                                                                                                                                                                          C. pneumoniae CT622 homologue CPn0728.
                                                                                                                                                                                                                                                                                       Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU38899 standard;
                      Disclosure; Page 161-162;
                                                         New polynucleotide for treating Chlamydia polynucleotides containing an immunogenic
                                                                                               N-PSDB; AAS57031.
                                                                                                                                  Bhatia
                                                                                                                                                                               21-APR-2000; 2000US-198853P
20-JUL-2000; 2000US-219752P
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                                                                                                                                                                                                                                                                                                                 coronary heart disease.
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                                                                                                          2001-616771/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLVNIGSLYSGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLVNIASLFSGYL 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVSRSGIESQGRSADASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQANQEEIM 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K---AAGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAGVPPAAASSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQIAEAQKK---FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSS
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               ABB90532
                                            ABB90532 standard; Protein;
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                                                                                                                      VLVNIGSLYSGYL
                                                                                                                                                                                                                                                                                                      GSSVKQLYKT--SKSTGSDYKTQISAGYDAYKSINDAYGRARNDATRDVINNVSTPALTR
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                                                                                                                                                 VLVNIASLFSGYL
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                                                                                                                                                                                                               QKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAFIQQ
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                                                                                                                                                                                                                                                CC pneumoniae (strain CML029), and ABLJ4184-ABLJ4183 represent DNA encoding Ct them. The proteins are predicted to be immunogenic and may therefore be CC useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is CC also involved in the development of cardiovascular diseases such as CC atherosclerosis, coronary artery disease, carotid artery stenosis, CM yocardial inferction, cerebrovascular disease, aortid anterysm, CC myocardial inferction, cerebrovascular disease, aortid anterysm, CC claudication and stroke. The proteins and nucleic acids of the invention CC may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched CC DNA probe assay or blotting techniques for determining Chlamydia CC specifically claimed Chlamydia pneumoniae protein of the invention.
                                                                                                                                                                            Query Match
Best Local S
Matches 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2000;
11-JUL-2000;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes .
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18-AUG-2000;
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22-DEC-2000;
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                 122
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                                                                                                              6
                                                                                                                              GPESVSSNQSSMNPIINGQIASNSETKESTKA----SEASP--SASSSVSSWSFLSSAK
KTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTID------
                                               NALMSLADKLGIASSNSSSSTSRS-ADVDSTTATAPTPPPPTFDDYKTQAQTAYDTIFTS 124
                                                                NALISLRD--AILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAKSGLENA 121
                                                                                                             GPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAV
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233; Conserv
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%; Pred. No. 8.4e-46;
126; Mismatches 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent novel proteins from Chlamy and ABL91184-ABL91373 represent DNA
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RESULT 11
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23-APR-2001;
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                                                treatment
                                                                                 Novel compositions comprising Chlamydia Capl protein and
                                                                                                                                                             WPI; 2002-179901/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 kDa protein; bactericidal; diagnosis; prevention; pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever;
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30-JUN-1999;
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                NAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKV
                                                                                                                                              ISLRD--AILNKNSSPTDSLSQLEASTSTSTYTRVAAKDYDEAKSNFDTAKSGLENAKTL 124
                                                                                                     AEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTID------KLNK
                                                                                       ADIQAALVSLQDAVTNIKDTAATD-----EET----AIAAEWETKNADAVKVGAQITE
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  SLVDQTDATATQIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQI
                                            LAKYASDNQAILDSLGKLTSFDLLQAALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQ
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99US-0141276
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Chlamydia
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prevention and treatment of C. pneumoniae (e.g. pneumonia, upper respiratory

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RESULT 14
AAY71957
ID AAY71
XX
AC AAY7:
XX
DT 26-M
XX
DT 26-M
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OR 76 |
KW 76 |
KW 76 |
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Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                             76 kDa protein; bactericidal; diagnosis; prevention; pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; treatment; fusion protein; truncation mutan:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
               09-NOV-2000.
                                                                                                                                          Synthetic
                                                                                                                                                       Chlamydia
                                                                                                                                                                                    mutein.
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                                                                                                                                                                                                                                                                    pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NALISLRD---AILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAKSGLENA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQIAEAQKK---FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTID-----K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPS-GSDIPIVGPS-GSAASAGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDQLVGADGELPAEIQAIKDALAQAL-KQPSADGLATAMGQVAFAAAKVGG 458
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                                                                                                Location/Qualifiers 453..490
                                                                      the C.
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Pred. No. 2e-19;
                                                                                                                                                                                                                                                                  truncation mutant
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                                                                   e sequence is
kDa protein"
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AAY35358
ID AAY3
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AC AAY3
XX

standard;

Protein;

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AAY35358;

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tract disease, bronchitis, sinusicis, considerate and disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases caused by C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a fusion protein comprising a truncated Chlamydia pneumoniae 76 kDa protein is used in the residues. C. pneumoniae 76 kDa protein is used in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory tract disease, bronchitis, sinusitis and acute respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding a 76 kDa useful for vaccinating against (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-1999;
30-JUN-1999;
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404
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 K---AAGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAG
                                                                    AGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAM
                                                                                                                         TKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPS-GSDIPIVGPS-GSAASAGSA
                                                                                                                                                                                LNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNI---SYEA
                                                                                                                                                                                                                                                                            TSLADIQAALVSLQDAVTNIKDTAATD-----
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                         SDQLVGADGELPAEIQAIKDALAQAL-KQPSADGLATAMGQVAFAAAKVGG
                                                      IGSI-----
                                                                                                          TQIAEAQKK---FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSS
                                                                                                                                                                 IAQSLVDQTDATATQIEKDGNAIRDAYFAGQNASGAYENAKSNNSISNIDSAKAAIATAK
                                                                                                                                                                                                                     ITELAKYASDNQAILDSLGKLTSFDLLQAALLQSVANNNKAAELLKEMQDNPVVPGKTPA
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99US-0141276
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28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       94; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 453; DB 21;
Pred. No. 2.3e-19;
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Chlamydia infections -
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                                                                                                                                                                                                                                                                            -EET----AIAAEWETKNADAVKVGAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 490;
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                 GPESVSSNQSSMNPIINGQIASNSETKESTKA----SEASP--SASSSVSSWSFLSSAK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1156; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-357842/30
AGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAM
                                                             TKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPS-GSDIPIVGPS-GSAASAGSA
                                                                                                                                   VLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAE
                                                                                                                                                                                               LNKLYTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNI---SYEA
                                                                                                                                                                                                                            TSLADIQAALVSLQDAVTNIKDTAATD-----EET----AIAAEWETKNADAVKVGAQ
                                                                                                                                                                                                                                                          KTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTID-----K
                                                                                                                                                                                                                                                                                                                      NALISLRD---AILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAKSGLENA 121
                                                                                                                                                                                                                                                                                                                                                    GPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAV
                                             TQIAEAQKK----FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSS
                                                                                                       IAQSLVDQTDATATQIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK
                                                                                                                                                                 ITELAKYASDNQAILDSLGKLTSFDLLQAALLQSVANNNKAAELLKEMQDNPVVPGKTPA
                                                                                                                                                                                                                                                                                        NALMSLADKLGIASSNSSSSTSRS-ADVDSTTATAPTPPPPTFDDYKTQAQTAYDTIFTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epitope.
                                                                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 451; DB 20;
Pred. No. 2.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               189;
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RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sinusitis; purulent otitis media;
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                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Page 1155; Disclosure; 1912pp;
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21-NOV-1997;
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                                                                          63
                                                                                                                                                                                     Local
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AESQENAFRKQPAFIQQVLVNIASLFSGYL 659
                                     FAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ×--
                        VMQIIQSNPQANNEEIRQKLTSAVTKPPQFGYPYVQLSNDSTQKFIAKLESLFAEGSRTA
                                                                          DATRDVINNVSTPALTRSVPRARTEARG-PEKTDQALARVISGNSRTLGDVYSQVSALQS
                                                                                       FVSAGVPPAAASSIGS----SVNQLYKT--SKSTGSDYKTQISAGYDAYKSINDAYGRARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDQLVGADGELPAEIQAIKDALAQAL-KQPSADGLATAMGQVAFAA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGSI-----RVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAA
                                                                                                                                                                           100;
                                                                                                                                                                         Similarity 47.6
00; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neutralising
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                                                                                                                                                                                                                           212
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97FR-0014673
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                                                                                                                                                                                       13.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumonia; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epitope.
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                                                                                                                                                                                     Score 445.5;
Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                             pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heart disease; sarcoidosis;
                                                                                                                                                                           69;
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RESULT 17
AAU37120
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                     Matches
                                 Query Match
Best Local
                                                                                                   for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are generichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Entercoccus faccalis. The invention is also useful for the identification of potential new targets
                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck
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                                                                                          ftp.wipo.int/pub/published_pct_sequences
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27-NOV-2000;
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ESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALIS
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DB; AAS54979.
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                                   Similarity
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                                                                    2344 AA;
                      Conservative
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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Xu HH;
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                                 8.0%;
21.1%;
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                      124;
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                    Score 256; DB 22;
Pred. No. 1.4e-06;
4; Mismatches 307;
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89
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                                                                                                                            Staphylococcus
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21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
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                                                                                                     21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus cellular proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSR 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSTSASTSTSMRTSTLDSQSMSLSTSTSTSVSDSTSLSDSVSDSTSDSTSTSTSGSMSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQA---LKQPSADGLAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLLSNSASASESDSSSTSLSDSTSASMQSSESDSQSTSTSLS-----NSQSTSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SISKSTSQSGSTSTSASLSGSESESDSQSISTSTSESKSESTSTSLSDSTSTSNSGSAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVKKAEEQI-----SQAQKDIQEIKPSG-----SDIPIVGPSGSA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSASMNQSGVDSNSASQSASTSTSTSTSESDSQSTSS-YTSQSTSQSESTSTSTSLSDST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSLT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAKSGLENAKTLAEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGQAL-QSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSP
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                                                                                                                                                                                                                                                                prokaryotic cellular
; antibacterial; drug
2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                            aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         6281
                                                                                                                                                                                                                                                                    proliferation protein;
design.
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                                                                                                                                                                                                                                                                                                                              protein #1573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential to C prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The collection is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Seq ID No 12996; 511pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-)
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                   370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 ESTKASEASPSASSSVSSWSFLSSAKNALISLRDAILNKNSSPTDSLS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides for the identification and development lbiotics, comprise sequences of antisense nucleic acids
                                                 GNFVNADTDKQNAYNNAVAHAEQIISGTPNANVDPQQVAQALQQVNQAKGDLN-----G
                                                                                                                                                                                    AVSHAEGILSKA----NGSNASQTEVEQAMQRVNEAKQALNGNDNVQRAKDAAKQVITNA
                                                                                                                                                                                                                                                         QVEQAPDIATVNNVKQNAQNLNNAMTNLNNALQDKTETLNS---INFTDADQAKKDAYTN
                                                                                                                                                                                                                                                                                    TIDKLNKLVTLQN--QN-KSLTEVLKTTDSA--DQIPAINSQLEINKNSADQIIKDLERQ
                                                                                                                                                                                                                                                                                                                                                                                                                    ---QLEASTSTSTYTRV------AAKDYDEAKSNFDTAKSGLENAKTLAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EITAALNKVTQAKNDLNGNTNLATAKQNVQHAIDQLPNLNQAQRDEYSKQITQATLVPNV 3285
NEMAAIALQGERSMIEQF-NVNNP-ATAKELQAMEAQLTA-----MSDQLVGADGELP 420
                                                                                                                   NDLNQAQKDALKQQVDAAQTVANVNTIKQTAQDL-----NQAMTQLKQGIADKDQTKAN
                                                                                                                                         PD-NIA---ATKELIDAAET--KVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPS
                                                                                                                                                                                                                                                                                                                         TTNPTMDPNTIQQALTKVNDTNQALNGNQKLADAKQDAKTTLGTLDHLNDAQK--QALTT
                                                                                                                                                                                                                                                                                                                                                                                             NAIQQAATTLNDAMTQLKQGIANKAQIKGSENYHDADTDKQTA---YDNAVTKAEELLKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-611495/70
                                                                                                                                                                                                                     NISY-EAVLTNAGEVIKASSEAGIKLGQALQSIVDA-----GDQSQAAVLQAQQ--NNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 7.9%;
Similarity 21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                           ----YETKMADLMAALQDMERLANSDPSNNHT----EEVNNIKKALEAQKD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 254; DB 22;
Pred. No. 6.6e-06;
                                                                     ·IVGPSGSAASAGSAAGALKSSNNS-GRISLLLDDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6281;
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                                               useful in
benefits
microbes
                                                                                                                                                                                            (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                     Enzyme; flavour; aroma; texture; nutritional; dairy manufacture; therapy; fermentation process; anti-infection; rotavirus infection; heart disease; infantile diarrhoea; lactose digestion; anti-cancer; autoimmune disorder; anti-mutagenesis; immune system modulation; allergy; Helicobacter pylori; antihypertensive effect; urogenical infection; hepatic encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3945
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                                                   New polynucleotides and polypeptides from Lactobacillus rhamnosus, useful in e.g. improving the flavor, aroma, texture and health-related benefits of milk-derived products, or in increasing properties of microbes -
                                                                                                                N-PSDB;
                                                                                                                                                                    Glenn M,
                                                                                                                                                                                                                                  08-AUG-2000;
28-NOV-2000;
                         Claim
                                                                                                                                                       Christensson
                                                                                                                                                                                                                                                                        08-AUG-2001;
                                                                                                                                                                                                                                                                                                                            WO200212506-A1
                                                                                                                                                                                                                                                                                                                                                    Lactobacillus rhamnosus HN001.
                                                                                                                                                                                                                                                                                                                                                                                           bowel syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactobacillus rhamnosus outer membrane protein rompA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE20110;
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                                                                                                                2002-241760/29.
DB; AAD31881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEITRALTQVTDAKNGLNGEAKLATEKQNAKDAVSGMTHLNDAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDALNGDEKLAQAKQEALANLDTLRDLNQPQRDALRNQINQAQALATVEQTKQNAQNVNT 3801
                        2:
                                                                                                                                                                                            GENESIS RES & DEV CORP
VIALACTIA BIOSCIENCE NZ
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                        Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                    Havukkala
                       64; 257pp; English
                                                                                                                                                                                                                                                                        2001WO-NZ00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                  2000US-0634238.
2000US-0724623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQENAFRKQPAFIQQVL 648
                                                                                                                                                                                                                                                                                                                                                                                          endocarditis; transgenic microbe; outer membrane protein.
                                                                                                                                                      Holland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQALKGQIDQSPEIATVNQVKQTATSLDQAMDQLSQAINDKAQTLA
                                                                                                                                                                    IJ,
                                                                                                                                                                  Bloksberg
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                                                                                                                                                      ₽₩,
                                                                                                                                                      Lubbers
W, Reid
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                                                                                                                                                      Dekker J;
Coolbear
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The

present invention relates to a

new isolated polynucleotide comprising

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                         1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lipids and prevention of heart disease; antihypertensive effect; prevention and treatment of urogenical infections, Helicobacter pylori, or hepatic encephalopathy; treatment of inflammatory bowel disorder and irritable bowel syndrome; modulation of endocarditis; and for improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diarrhoea; aid in lactose digestion; as anti-cancer and anti-mutagenesis; liver cancer reduction; reduction of small bowel bacterial overgrowth; immune system modulation and treatment of autoimmune disorders and allergies; treatment of allergic responses to foods; reduction of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1052
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ASVASSAASAASSAAKAGNSSAAGTYSHAASAAASSAKSAESQASSAASAAASDDS
                                                                                                                                                                                                                                                                                                                                                                                                   VASSA----ASAAAGFDKAASA-AEGAASSAASAASSAAAQGTRGGASSSASEAGQAST- 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAVSNADASANSAAAAYDSYAS-EASAAS-----AANDSSGYATASFAASSAAAAMSA 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NALISLRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKD---YDEAKSNFDTAKSGLEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HADNMEI -- KSLASDAEKQSQI -- ALAASKSAAASSSAAASAAIVASSAASE---- ASSA 802
                                                                 ANQEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQEN 635
                                                                                                                                  RYPSDSGIQSDVSIASSAASTASSAASAAQSEASTASSAASHASEQASIASSEDVVSSSA
                                                                                                                                                                                                                                                                    ---ATSVYASAASSSASEAGSYAHQAGSSA-----SEATGHASSATSQASAASSAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGS-----AGTAGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASATKAG------DSKAAA----GFSSAASA--AASSAKGAEAVASEAASAASDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQL 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAKASSNASAATSAAAVG-----FSAASDASEQAKTAASADVVA-SSAASTANSNASAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGAL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AASSSASEAGSYAHQAGSSASDAVGQSGSAAQHASTAASAASSYPKDSGTQSLASQAASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVIKASSEAGIKLGQALQSIVDA----GDQSQAAVLQAQQNNSPDNIAATKELIDAAETK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALSTAQVAAKVAVSDAAAAGSAAAVASAAQSDSKNKQA-----TAATARSQALDDLNK
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                                                                                                                                                                                                   RSVSRSGIESQ----GRSADASQRAAETIVRDSQTLGDVYSRLQVLDSLMST--IVSNPQ
                                                                                                                                                                                                                                                                                                                              QMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQ--TANPALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KSLTDYASGASS-----SASEAGQAST---
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Pred. No. 1
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1.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                             AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the scepidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                    1100
                                                                                                                                                                                                                                                                          ÀAH55098 represent oligonucleotide sequences and primers which are use in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 447 no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-316495/33.
N-PSDB; AAH53785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001
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 104
                                                                    61
                                                                                                                                                                                         Local Similarity
                                                                                                                                       1 MHHHHHHMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLS
                                                                  SAKNALISLRDAILNKNSSPTD---SLSQLEASTSTVTRVAAKD------
                                                                                                      VNNAQHVIDETQATLSSD--TINQLANAVTQAKSNLHGDTKLQHDKDSAKQTIAQLQNLN
                                    SAQK---HMEDSLIDNESTRTQVQHDLTEAQALDGLMGALKESIKDNTNIVSNGNYINAE 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 779-781;
                                                                                                                                                                                                                                          5024 AA;
                                                                                                                                                                           Conservative
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                                                                                                                                                                         130;
                                                                                                                                                                                       Score 249.5; DB 22;
Pred. No. 9.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frame protein sequence
 -KSNFDTAKSGLENAKTLAEYETKMADLMAALQD 140
                                                                                                                                                                         Mismatches 247;
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                                                                                                                                                                                                         Length 5024;
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                                      Doucette-Stamm
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                                                                                                             14-AUG-1997;
08-NOV-1997;
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                                                                      (GENO-) GENOME
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gene therapy
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97US-064964P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                therapy
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                                                                                                                                                                                                                                                                                                                                 reading frame;
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                                                                                                                                                                                                                                                                                                                                                                     acid sequence SEQ ID NO:3159
                                                                                                                                                                                                                                                                                                                                 ORF; bacterial infection;
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Best Local Similarity
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                   AKQLNGDMSTLHK----
                                                     MQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRK 639
                                                                                                                                                                                                                                         AEKLKE -- AEALDEAM ----
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19.7%;
                 -VINDKDQIQHLS-----NYINADNDKKQNYDNAIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128;
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Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections

ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABp35124 to ABB37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the

NQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRDAILNKN Score 248.5; DB : Pred. No. 2.7e-05 Mismatches 23; Indels 189; Length 10182; Gaps 77 31;

SSDTINQLANAVTQAKSNLHGDTKLQHDKDSAKQTIAQLQNLNSAQK---HMEDSLIDNE QTSSTELDGLTDLTDAQREKLREQINTSNSRDDIKQKIEQAKALNDA--MKKLKEQV--A -----QRVETIINETQNPELLKAN------IDQATQSVQNA----EQALHGAEKLNQDK 6283 KTLAEYET-KMADLMAALQDMERLANS-----DPSNNHTEEVNNIKKALEAQKD---SSPTD---SLSQLEASTSTSTVTRVAAKDYDEAKSN-------FDTAKSGLENA 121 IKDLERONISYEAVLTNAGEVIKASSEAGIKLGOALOSIVDAGDQSOAAVLQAQONNSPD NLVNSASTLEQVQQNLQTAQQLDNAMGELRQSTAKKDQVKADSKYLNEDPQTKQNYDDAV -----TIDKLNK-LYTLQNQNKSLTEVLKTTDSADQIPA----INSQLEINKNSADQI 217 INGTNQPTINKGNVTTATQTVKNTKDALDGDHRLEEAKNNANQTIRNLSNLNNAQKDAEK STRTQVQHDLTEAQALDGLMGALKESIKDYTNIVSNGNYINAEPSKKQAYDAAVQNAQNI 6339 6239 6179 169 6119 6059 319 277

KQAQDNLHGAQKLQQDKNTTNQAIGNLNHLNQPQKDALIQAINGATS-----RDQV QKDGVH---ANSDY----TNEDSAQKDAYNNALKQAEDIINNSSNPNLNAQDITNALNNI QKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSS----NNSGRISLLLDDVDNEMAAI QNIKDAVNNLHGDQKLAQSKQDANNQLNHLDDLTEEQKNHFKPLINNADTRDEVNKQLEI INEDSDKQKT----YNDKIQAAKEIINQTSNPTLDK---LSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQRAAETI AQALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAA 490 A-----LQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDAL 430 SQTLGDVYSRLQVLDSL-----MSTIVSNPQANQE-----EI ----QKIADTL -KQLEDQVNQDDQISNSSPF 6575 585 6515 550 6476 6443 6392 375

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RESULT 22
AAU37018
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                                                                                                                 Matches
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                            The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a side verifier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                           a wide variety of organisms. The present sequence represents essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                 Sequence
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Yamamoto RT,
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                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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 43
                            10
                           SGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKN----
TGTPDVVVTPSEITAALNKVTQAKNDLNGNTNLATAKQNVQHAIDQLPNLNQAQRDEYSK
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                                                           167;
                                                                        Similarity
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                         Conservative
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Xu HH;
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                                                                     7.7%;
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                                                      Score 247; DB 22;
Pred. No. 7e-06;
44; Mismatches 285;
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AC AAU7
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                                                                                                                                                          Antigenic protein; vaccine; SEREX; antibacterial; antiinflammatory; dermatological; antilucer; tuberculostatic; immunosuppressive; septicaemia; food poisoning; skin disorders; peritonitis; endocarditis; tuberculosis; blood infection; sepsis; meningitis; pneumonia; stomach ulcer; gonorrhea; necrotising fasc
                                                               Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                          S. aureus antigenic protein associated protein #9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                            Lyme's disease; gastro-enteritis; dysentery; shigellosis.
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Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 medicament for treating Staphylococcus aureus-associated septicaemia, food poisoning or skin disorders or Staphylococcus epidermidis-associated septicemia, peritonitis, endocarditis, tuberculosis, blood infections, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhea, necrotising fasciitis, impetigo, Lyme's disease, gastro-enteritis, dysentery and shigellosis. The present sequence is an S. aureus protein sequence associated with the antigenic proteins of the invention.

Note: The present sequence is included in the sequence listing but is not mentioned anywhere else in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the library into host cells, contacting the polypeptides expressed by the genes with autologous antisera derived from an animal infected with, or has been infected with the pathogen and purifying the nucleic acid encoding the polypeptide or partial polypeptide binding to the antisera. Also included are the nucleic acids and polypeptides isolated by the method, vectors and transformed cells expressing them, vaccine comprising the polypeptide and the production of monoclonal antibodies against the polypeptides. The protein and vaccine are useful
                                                                                                                                                                                                                                 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed by pathogenic organisms e.g., Staphylococcus aureus infection, by SEREX (serological identification of antigens by recombinant expression cloning) techniques. The method involves providing a nucleic acid library encoding genes/partial gene sequences of pathogenic organisms, transforming/transfecting the library and the best collaboration transferring the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying antigenic polypeptides expressed by pathogenic organisms e.g., Staphylococcus aureus during infection, by SEREX (serological identification of antigens by recombinant expression cloning)
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                                                                            1949
                                                                                                                                                                                                                                                                                                              1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for identifying antigenic polypeptides
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                                                                                                                                                         1892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ibodies against the polypeptides. The protein and vaccine are useful immunising an animal (preferably human) against a pathogenic microbe proteins and antibodies are useful for manufacturing a
QAKQTAKQQLNNMTHLTTAQKTNLTN--QINSGTTVAGVQTVQSNANTLDQAMNTLRQSI
                                    --KNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIK-----LGQAL----QSI
                                                                                                                                                                                                                                                                                                                                                HMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNAL
                                                                        NIK----KALEAQKDTIDKLNKLYTLQNQNKSLTEVLKTTDSADQIPAINSQLEIN----
                                                                                                                                                     AQKADVKSKINAASNIAGVNTVKQQGTDLNTAMGNLQGAINDEQTTLN---SQNYQDATP
                                                                                                                                                                                         -----KSGLENAKTLA-----
                                                                                                                                                                                                                               VSSAETII NQTTNPTMSVDDVNRATSAVTSNKNALNGYEKLAQSKTDAARAIDALPHLNN
                                                                                                                                                                                                                                                                     ISLRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDE-AKSNFDTA------
                                                                                                                                                                                                                                                                                                          HQIDAVNTIKQNATNLNSAM-GNLRQAVADKDQVKRTEDYADADTA-----KQNAYNSA 1831
                                                                                                                                                                                                                                                                                                                                                                                          157;
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                                                                                                                                                                                                                                                                                                                                                                                        137;
                                                                                                                                                                                                                                                                                                                                                                                      Score 244.5; DB 23;
Pred. No. 7.9e-06;
17; Mismatches 285;
                                                                                                                                                                                         -EYETKMADLMAALQDMERLANSDPSNNHTEEVN
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RESULT 24
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
WPI; 2001-611495/70
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                      Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                       Staphylococcus
                                                                                                                                                                                                                                                                               antibiotic;
                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus cellular proliferation protein #615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAALQRVNN--AKDALNGDAKLIAAQNAAKQHLGTLTHITTAQRNDLTNQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLDQAMASLQNGINNESQVKSSEKYRDADTNKQQEYDNAITAAKAILNKSTGPNTAQNAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QISQAQKDIQ------EIKPS----GSDIPIVGPSGSAASAGSAAGALKSSNNSGR--I 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNGDENLAAAKQ----NAKTYLNTL----TSITDAQKNNLISQITSATRVSGVDTVKQNAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAETI-----LNKQTGPNTAKTAVEQALNNVNNAKHALNGT-QNLNNAKQAAITAINGA
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                                                          ELITRA PHARM
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; antibacterial; drug design.
                                                                               2000US-206848P
2000US-207727P
2000US-242578P
2000US-253625P
2000US-257931P
2001US-269308P
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                      Ohlsen
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for identification development. The autisense nucleic acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                             2191
2289 DADQAKQQAYNTAVTNA---ENIISKANGGNATQAEVEQAIKQVNAAKQALNGNANVQHA 2345
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                                                                                                                                                                                                                                                                                                   391
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                                                   511 GVQSAISQTANPALSRSVSRSGIESQGRSADASQRAAETIVRD----SQTLGDVYSRLQV
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                                                                                                                                                                                                                                                                                                                                                             LDPTVI - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NANOSQVEAALSTYTTTKOALNGDRKVTDAKNNANQTLSTLDNLNNAQKGAVTGNINQAH
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                                                                                                                                                                       FAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRS
                                                                                                                                                                                                                                                                                          NPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVA
                                                                                                                                                                                                                                                                                                                                                                                                                 SDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAATKELIDAAETKV-----NELKQEHTGLTDSPLVKK--AEEQISQAQKDIQEIKPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQHANTAIDGLSHLTNAQK --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LERQNISYEAV--LTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAQKDTIDKLNKLVTLQNQNKSL-TEVLKTTDSADQIPAINSQLEINK---NSADQIIKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDSLSQLEASTSTSTVTRVAA---KDYDEAKSNFDTAKSGLEN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NVDAAMDKLRQSIADNATTKQNQNYTDASQNKKDAYNNAVTTAQGIIDQTTSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AKTLAEYETKMADLMAALQD-----MERLANSDP--SNNHTEEVNNIKKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NKSTGTNVPK-----DQVEAAMNQVNATKAALNGTQNLEKA
                                                                                                                                                                                                                                   -AQKQTVTDQINGA------HTVDE--ANQIKQ-NAQNLNTAMG---
                                                                                                                                                                                                                                                                                                                                                       ---NQAAGQVSTTKNA-----LNGNEN-LEAAKQQASQSLGSLDNLN
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Pred. No. 1.
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1.4e-05;
hes 222;
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                                                                                                                                                           Matches 136;
                                                                                                                                                                                        Query Match
                                                                                            1079
                                                                                                                                                                                                                                                                                                           ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2403
                                                                                                                                                                                                                                                                 cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID 4463; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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08-NOV-1997;
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121 AKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVTL 180
                                                              61
                                                                                                                            9
                                                                                                                                                                         Local Similarity
                                 TSESASTSTSES - - ESNSASTSLSGSLSTSISDSTSTSTS - - - - DSASTS - - TSESESDS
                                                              SAKNALISLRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAKSGLEN 120
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                                                                                            ESDSTSTSLSESTSTSLSGSTSASTSDSASTSTSESDSTSESTSLSESLSTSVSDSTSAS
                                                                                                                           ESGPESVSSNQSSMNPIINGQIASNSE----TKESTKASEA---SPSASSSVSSWSFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN92163
                                                                                                                                                                                                                                                    site.
                                                                                                                                                                                                                    2137 AA;
                                                                                                                                                         Conservative 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THERAPEUTICS CORP
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97US-064964P.
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                                                                                                                                                        Score 237; DB 23;
Pred. No. 1.7e-05;
34; Mismatches 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2137
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                                                                                                                                                           Indels
                                                                                                                                                           96;
                                                                                                                                                         Gaps
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RESULT 26
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23-MAY-2000;
26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                        Haselbeck R, Yamamoto RT,
                                                                                                         (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus cellular proliferation protein #688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMEAQLTAMSDOLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVG-G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STSDSASASTSESDSDS···ASTSSSESVSTSVSDSTSASTSES----ASTSTSVSDS
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                                                                                                                                                     ; 2000US-191078P.
; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
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                           Ohlsen KL,
Xu HH;
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DR N-PSDB; AAS52271.

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New polynucleotides for the identification and development of printibiotics, comprise sequences of antisense nucleic acids - artibiotics, comprise sequences of antisense nucleic acids - artibiotics, comprise sequences of antisense nucleic acids - xx

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Example 3; Seq ID No 5908; 511pp; English.

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Example 3; Seq ID No 5908; 511pp; English.

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Example 3; Seq ID No 5908; 511pp; English.

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Example 3; Seq ID No 5908; 511pp; English.

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Example 3; Seq ID No 5908; 511pp; English.

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Example 3; Seq ID No 5908; 511pp; English.

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Example 4; Pather 1 seq Intervention, their use inhibitions of question in the proliferation in the proliferation in the proliferation in the proliferation in the proliferat
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Š 밁 Q 밁 Qy В õ 밁 Qy В Ş 밁 Q Вр Ş ₽ Q 밁 Q Query Match Best Local S Matches 137 530 824 692 635 582 529 480 420 362 787 302 741 242 192 135 75 16 SSNQSSMNPIINGQIAS-NSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRDAIL 74 TDKQTAYNTAVNEAAAMINKQTGQNANQTEVEQAITKVQTTLQALNGDHNLQV-----RSGIESQGRSADASQRAAETI -----IAQAQALNEAM-KALKESIKDQPQT-------EASSKFINEDQAQKDA-PAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAF 479 ---LDGVER----LAQDKQTAGNSLNHLDQLTPAQQQALENQINNATTRDKV----AEI SLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQL--TAMSDQLVGADGEL GLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRI 361 AVKQDLTEAQALDQLMDALQQSIA-----DKDATRASSAYVNAEPNK----KQSY-SSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHT NTTKA----ALHGDVKLQND-----KDHAKQTVSQLAHLNNAQKHMEDTLIDSETTRT KTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNA------GEVIKA ROSIODNAATKANSKYINEDOPEQQNYDQAVQAANNIINE--QTATLDNNAINQAATTV-MAALQD-MERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQ--NKSLTEVL 191 ----AKTNATQAIDALTSLNDPQKTALKDQVTAATLVTAVHQIEQNANTLNQ---AMHGL NKNSSPTDSLSQLEASTSTSTSTVTRVAAKDYDEAKSNFDTAKSGLENAKTLAEYETKMADL SSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSV----Similarity -----DEAVQNAESIIAGLN-----NPTINKGNVSSATQAVISSKNA---Conservative 7.4%; Score 236; DB 22; 20.1%; Pred. No. 9.2e-06; tive 123; Mismatches 239; -YTQAVQHAKDLINKTTDPTLAKSIIDQATQAVTDA -VRDSQTLGDVYSRL---QVLDS Length 1215; 184; S----Gaps 419 569 946 529 911 871 823 301 740 241 634 134 581 27;

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KNNLHGDQKLAQDKQRATETLNNLSNLNTPQRQALENQINNAATRGEVAQKLTEAQALNQ 1006

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RESULT 27
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                                                                                                                                                                                         The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
                                                                       for homologous nucleic acids which are required for cell proliferation a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
                                                                                                                              to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen
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                                           of the printed specification, but was obtained in electronic format directly from WIPO at
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27-NOV-2000;
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26-MAY-2000;
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                             .int/pub/published_pct_sequences
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                                                                        Staphylococcus
                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                   Staphylococcus aureus cellular proliferation protein #614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AKTNATQAIDALTSLNDPQKTALKDQVTAATLVTAVHQIEQNANTLNQ----AMHGL
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Note: The sequence data for this patent did not form part
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Best Local Similarity
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27-NOV-2000;
22-DEC-2000;
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26-MAY-2000;
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EKQALKDRINQILQQGHNGINNAMTKEEIEQAKAQLAQALQDIKDLVKAKEDAK-----
                               LIDAAETKVNE-LKQEHTGLTDSPL---VKKAEEQISQAQKDIQEIKPSGSDIPIVGPSG
                                                                                                                                                             TLQNQNKSLTEVLKTTDSA-----DQIPAINSQLE-----INKNSADQIIKDLERQ-
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                                                                                                                             AIQSINQALANKLKEIEASNATDQDKLIAKNKAEELANSIINNINKATSNQAESQVQTAG
                                                                                                                                                                                                                                                                                            RDAILNKNSSPTDSLSQL---EASTSTSTYTRVAAKDYDEAKSNEDTAKSGLENAKTLAE 126
                                                                                             NISYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKE
                                                                                                                                                                                                                              YETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLN------KLV 178
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                  7.48;
20.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 235.5; DB : Pred. No. 2.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was
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RESULT 29
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                                                  agricultural applications, and advantageous strain improvements based on genetically engineering a Gram-positive microorganism to delete, underexpress or overexpress the enzyme. Due to overall relatedness of the enzyme with Pseudomonas lasa protein, YOMI appears to be a member of the M23 metalloprotease family. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1770
          also be used for peptide hydrolysis, waste treatment and
                         metalloprotease can be used in claimed cleaning compositions, animal feed and compositions for the treatment of textiles.
                                                                                                                         The invention relates to the discovery of this previously unknown metalloprotease, uses of the metalloprotease in industrial and
                                                                                                                                                     The present sequence is metalloprotease YOMI of Bacillus subtilis
                                                                                                                                                                                 Claim 4; Fig 1A-O; 59pp; English
                                                                                                                                                                                                              microorganism
                                                                                                                                                                                                                                                                                                   Estell DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9914342-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gram-positive bacterium
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                                                                                                                                                                                                                           Compositions containing metalloprotease from Gram-positive
                                                                                                                                                                                                                                                         N-PSDB; AAX24980
                                                                                                                                                                                                                                                                                                                                                                         15-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOMI; metalloprotease; protease; textile; animal feed; detergent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW98149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-----NPDLTPEQKAKAL----KEIDEAEKRALQNVENAQTIDQLNRGLNLGLDDIRN
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising a nucleic acid (see AAX24980) encoding the metalloprotease and host cells are claimed. Gram-positive cells in which YOMI is inactivated (by gene mutation or deletion) are used for production of heterologous proteins, especially enzymes, hormones, growth
            AAU34389
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                                                             YKELQKVKESRSLTSDEEQEYLQ---VTQQLAQTFPALVKGY
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                                                                                                      GAFAALGWALESLISSFAEAKKAKDD-
                                                                                                                                             TLLLSKNTRTLASSLILGTRAMGQETLATAGLEAGMTRAAVASRVLKTALRGLLVSTLVG
                                                                                                                                                                                                                                                                                                                                K-SSNNSGRISLLLDDVDNEMAAIALQ-------GFRSMI----
                                                                                                                                                                                                                                                                                                                                                   SNKITDILQMTGDFGRMGFDESELSTLTKTAQVLQ----NVSDLTPDDTVNTLTAAMLNF
                                                                                                                                                                                                                                                                                                                                                                                                              D------QSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPL
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                                                                                 L-EREFVDGERSLAESQENAFRKQPAFIQQVLVNIASLFSGY
                                                                                                                        DVYSRL-QVLDSLMSTIVSNPQANQEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQ
                                                                                                                                                                                     NKLQNNFTEFAIAASDAF---ISDGLIEFTQAAGSLLNASTGVIKSVGFLPPLLAAVSTA
                                                                                                                                                                                                       KQLYK--TAFSSTSSSSYAAALSDGYSAY-KTLNSLYSESRSGVQS------AISQTA
                                                                                                                                                                                                                           SDAQKQNTSIGVAGIYQLSRFNAMMNNFSIAQNAAKTAANSTGSAWSEQQKYADSLQARV
                                                                                                                                                                                                                                                AQALKQPSADGLA-----AGTVQMNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIKKALEAQKDTIDKLNKL-------VTLQNQNKSLTEVLKTTDS---ADQIPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -RNTALKQETQEVNKLTQATEKLGQVQKKTVQRNLQGQPTKVVQKNRHGFDDIVYTTDPK
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            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytokines.
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           Protein;
                                                                                                                                                                                                                                                                                       -NNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDAL
                                                                                                                                                                                                                                                                                                                                                                       -EEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141;
                                                                                                                                                                 ----SVSRSGIESQGRSADASQRAAETIVRD----SQTLG
           1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 235; DB 20; Pred. No. 2.4e-05;
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cc genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella Cc Invention is also useful for the identification of potential new targets Cc invention is also useful for the identification of potential new targets Cc for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, Cc and to obtain antibodies capable of binding to the expressed proteins. Cc The proteins can be used to screen compounds in rational drug discovery Cc programmes. The antisense nucleic acid sequence is also useful to screen Cc a wide variety of organisms. The present sequence cell proliferation in Cc assential prokaryotic cellular proliferation continued for cell protectic acid acid sequence represents an Cc of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids {\bf r}
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3;
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23-MAY-2000;
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                                                                       RDAILNKNSSP-----TDSLSQLEASTS-----TSTVTRVAAKDY------DEAK 108
                                                                                                                                 AGVQTVQSNANTLDQAMN-TLRQSIANKDATKASEDYVDANND-----KQTAYNNAVAA 241
                                              AETII INANSNPEMNPSTITQKAEQVNSSKTALNGDENLTAAKQNAKTYLNTLTSITDAQK
                                                                                                                                                                            SGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISL
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; antibacterial; drug design.
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Xu HH;
-DTAKSGLENAKTLAEY-ETKMADLMAALQDMERLANS---
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Pred. No. 9.1e-06;
2; Mismatches 288
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RESULT 31
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ID AAU37
XX AAU37
AC AAU37
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DT 14-FE
XX AN115
KW AN115
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XX Stapl
XX 27-SI
PR 21-MJ
PR 23-MJ
PR 23-MJ
PR 23-NJ
                      21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
23-OCT-2000;
27-NOV-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                         Staphylococcus
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Commoniae, proteins can be used to screen tequired for cell proliferation in the protein are required for cell prolif
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Best Local
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Yamamoto RT,
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DB; AAS55349.
LTAMSDQLVGADGELPAE--IQAIK------DALAQALKQPSADGLATAMGQVAFAAAK 455
                                                                LKHA---
                                                                                                                                                  LNNAKQAAITAINGASDLNQKQKDALKAQANGAQRVSNAQDV-----QHNATELNTAMGT
                                                                                                                                                                                          SPLVKKA-----EEQISQAQKDIQEIKPSGS-----DIPIVGPSGSAASAGSAAGA
                                                                                                                                                                                                                                     QNFLDADEQKRNAYNQAVSAAETILNKQTGPN---TAKTAVEQALNNVNNAKHALNGTQN
                                                                                                                                                                                                                                                                             QSIVDAGDQSQAAVLQA------QQNNSPDNIAATKELIDAAETKVNELKQEHTGLTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDAILNKNSSP-----TDSLSQLEASTS-----TSTVTRVAAKDY-----DEAK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGVQTVQSNANTLDQAMN-TLRQSIANKDATKASEDYVDANND-----KQTAYNNAVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISL 69
                                                                                                        LKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKEL---
                                                                                                                                                                                                                                                                                                                         LGTLTHITTAQRNDLTN--QISQATNLAGVESVKQNANSLDGAMGNLQTAINDKSGTLAS
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Xu HH;
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                                                                - IADKTNTLASSKYVNADSTKQNAYTTKVTNAEHIISGTPTVVTTPSE
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Pred. No. 9.3e-06;
2; Mismatches 288
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                                                                                                                     The invention relates to antisense inhibitors of genes essential to prokaryotic cellular prolliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haselbeck
Yamamoto I
                                              for antibiotic development. The antisense nucleic acids can also be us to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; antibiotic;
  programmes.
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27-NOV-2000;
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26-MAY-2000;
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                          The proteins
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
  The antisense
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                       can be used to screen compounds in rational drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for homologous nucleic acids which are required for cell proliferation a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                Lactococcus lactis IL1403
                                           Biosynthesis; biodegradation; lactic
                                                                        Lactococcus
                                                                                                     16-MAY-2002
                                                                                                                                ABB54168;
                                                                                                                                                             ABB54168 standard; Protein; 1063
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No. 4.4e-06;
                                             bacterium;
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                                          yogurt;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent is based on equivalent patent WOZ00177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production of yogurt and cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence useful in is and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                         VGNSSASASSAAVASFTAILATNPSMVPMLTQALAAAAPATTSGSAILNTTLGDLVNQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSSSSNDNGSNSILSSSNAADSVDSAVGSQSSTSSSGVLSESSAIDSGIASVSQSSEMNL
                                                                                                                                                                                                     KELIDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSG---
                                                                                                                                                                                                                                                                                                                                          QKDTIDKLNKLYTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNI
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PNNINNFVNNALNGITTIINSLTPSVGASTVNPNSSANSSQSSSSASSSSSAASSSTSSS
                                                                                                                        VLSPTLNNLTGASLGEVA-----NLTGVSSLLDQVNNSLGNLISLGSTALATIENTLQ
                                                                                                                                                                                    FDLDTLVSLQGNDLVNYLAGLVVNSAINRV-GQIAWSQ-----LSPTISNIPLVGTTVNN
                                                                                                                                                                                                                                                 SPAAMLTFLENPTIPGLSSIPGASL--VLSPVLSAISTVTSGIVN-QLNTTTSNALGGVN
                                                                                                                                                                                                                                                                              SYEAVLT -- NAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNI -- AAT
                                                                                                                                                                                                                                                                                                             -----AANPGAFLLNEIKS-----AGLDVSQIPLVGGQIAAAFNAI------PSM
                                                                                                                                                                                                                                                                                                                                                                           ST--VGISGLANIFSTLGTFNIPGMTTAAAALNGVEQIVNI------VGNIQEA---
                                                                                                                                                                                                                                                                                                                                                                                                      SNEDTAKSGLENA-KTLAEYETK-MADLMAALQDMERLANSDPSNNHTEEVNNIKKALEA
                                                            NSLNSFGNLPAGASDILNQVLNQLQNAINNIVESATGIVNNLPG-LGAIENGLSNTISQI
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                             --- PSADGLATAMGQVA----
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Pred. No. 1e-05;
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                           ---FAAAKVGGGSAGTAGTVQM
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Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumonlae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3;
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27-NOV-2000;
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DB; AAS52066.
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                                  Staphylococcus
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                                                                                                                  Staphylococcus aureus cellular proliferation protein #419
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                                                                                                                                                                                                                                                                                                                                                                            SVEEIQQQEQAHIEQFNPEQFTIEQAKSNAIKSIEDAIQHMIDEIKARTDLTDKEKQEAI 1649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQAIEQVHANEIPKAKIDANKDVDKQVQALI-------DEIGRNPNLT 1314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLN------KLV 178
                                                                                                                                                                                                                                                                                                                                                                                                          SQGRSADASQRAAETIVRDSQTLGDVYSR-LQVLDSLMSTIVSNPQANQEEIMQKLTASI 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TAFSSTSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIE
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41; Conservative
                                                                                   prokaryotic cellular
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                                    aureus
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19.8%; Pred. No. 2.7e-05;
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Best Local Similarity
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                            1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coll, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
                                   1450
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                                                                                                                                                                                                                                                                                                             1221 ILNKQTGSNSDKAAVDRALQQVTSTKDALNGDAKLAEAKAAAKQNLGTLNHITNAQRTAL 1280
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N-PSDB; AAS52002.
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 VDAGDQSQAAVLQAQQ------NNSPDNIA-----ATKELIDAAET----
                                   QNYLDASDS ---- NKN-----
                                                                                                                                                                                                           DTAKSGLENAKTLAEYETKMADL------MAALQDMERLANSDPSNNHTEEVNNIK 161
                                                                 ADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIKLGQALQSI 256
                                                                                                     NLTQLQKDNLKHQVEQAQNVAGVNGVKDKGNTLNTAMGALRTSIQNDNTTKT-----S
                                                                                                                                     KALEAQKDTI------DKLNKLVT-----LQNQNKSLTEVLKTTDS 196
                                                                                                                                                                         VTAAEGILNKQTGG--NTSKADVDNALNTVTRAKAALNGAENLRNTKTSATNT--INGLP
                                                                                                                                                                                                                                            EGQINQATTVDGVNTVKTNANTLDGAMNSLQGSINDKDATLRNQNYLDADESKRNAYTQA
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23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU37017;
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     Example 3; Seq ID No 12610; 511pp; English
                                                   New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                         Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                              23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU37017 standard; Protein;
                                                                                                                                                                                                                                                                              (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNAAKAILTKASGQNVDKAAVEQALQNVNSTKTALNGDAKLNEAKAAAKQTLGTLTHINN
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DB; AAS54876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQNLERA - - - - - - - KQAANTAITNASDLNTKQKEALKAQVTSAGRVS - - - - - AANGVEHTA
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                                                                                                                                                                                                                                                                              ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                          ; 2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-25362SP.
2000US-25931R.
2000US-25931R.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets of or antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen CC or homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3498 ILNKQTGSNSDKAAVDRALQQVTSTKDALNGDAKLAEAKAAAKQNLGTLNHITNAQRTAL 3557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLTQLQKDNLKHQVEQAQNVAGVNGVKDKGNTLNTAMGALRTSIQNDNTTKT-----S
  QTLGDVYSRLQ-----VLDSLMSTIVSNPQANQEEIM-QKLTA-----SISKAPQFGYPA 603
                                                                             IQNLERA-----KQAANTAITNASDLNTKQKEALKAQVTSAGRVS-----AANGVEHTA
                                                                                                                                                                            TAYSQAVNAAATI---------LNKTAGGNTPKADVERAMQAVTQANTALNG
                                                                                                                                                                                                                             TAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNS
                                                                                                                                                                                                                                                                            AQRTALDNEITQATNVEGVNTVKAKAQQLDGAMGQLETSIRDKDTTLQSQNYQDADDAKR 3989
                                                                                                                                                                                                                                                                                                                             VNNPATAKEL-QAMEAQ-----LTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLA
                                                                                                                                                                                                                                                                                                                                                                              VNAAKAILTKASGQNVDKAAVEQALQNVNSTKTALNGDAKLNEAKAAAKQTLGTLTHINN
                                                                                                                                                                                                                                                                                                                                                                                                                            GSAAGAL -- KSSN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVNELKQE----HTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAA--SA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANQVNTTKAALNGAQNLAQAKTTAKNNLNNLTSINNAQKDALTRSIDGATTVAGVNQETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNYLDASDS----NKN-----NYNTAVNNANGVINVTNNPNMD-ANAINGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTAKSGLENAKTLAEYETKMADL------MAALQDMERLANSDPSNNHTEEVNNIK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGQINQATTVDGVNTVKTNANTLDGAMNSLQGSINDKDATLRNQNYLDADESKRNAYTQA 3617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SLRDAI--LNKNSSPTD-SLSQLEASTS--TSTVTRVAAKDYDEAKSN----F 111
                                                                                                                           LYSESRSGVQSAISQTANPALS-----
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22.0%;
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                                                                                                                              -RSVSRSGIESQGRSADASQRAAETIVRDS
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Length 5795;

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Gaps

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                                                                                                                                                                                                                                                      AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the containing them which are used to produce hosts cells which express the polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria crivity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to CAAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH53091 to Sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465.
                                                                                                                        Matches
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                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kimmerly WJ;
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36; Mismatches
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23-MAY-2000; 2000US-206848P
26-MAY-2000; 2000US-207727P
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Conte: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                   SYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELI
                                                                                                                                                                                                                                                                                                                          KVTAAQQSKKVTQDEVAALVTKINNDKNNAIAEINKQTTAQGVTTEKDNGIAVLEQD--V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVEMNKDALQQQVNSQVDNSHYT
                                                                      SAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFN-VNNPATAKELQAMEAQL
                                                                                                          AEAIERINAAKV--SGV-----KAIEATTTAQ-DLERVK-----
                                                                                                                                             DAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAG
                                                                                                                                                                                QVEAIKTKAINDINQTTPATTAKAAALEEFDE------VVQAQIDQAPLNPDTTNEEV
                                                                                                                                                                                                                                                     ITPTVKPQAKQDIIQAVTTRKQQIKKSNASLQDEKDVANDKIGKIETKAIKDIDAATTNA
                                                                                                                                                                                                                                                                                     LTEVLKTTDSADQIPAI------NSQLEINKNSAD-----QIIKDLE--RQNI
                                                                                                                                                                                                                                                                                                                                                            LMAALQDMERLANSDP-----SNNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQNKS 186
                                                                                                                                                                                                                                                                                                                                                                                               LN------EDANHVKTANRASQADIDGLVTKLQAAL--IDNQAAIAELDTKAQE
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2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                     -NEETSKIENITDSTQTKMDA------YNEVKQAATARKAQNATVS-
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 222; DB 22;
Pred. No. 0.00016;
4; Mismatches 275;
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ucleic acids
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RESULT 39
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   В
                                          The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1082
for antibiotic development. The antisense nucleic acids can also be us to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discover
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibiotic;
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                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                             Yamamoto RT,
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16-FEB-
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic cellular proliferation protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus cellular proliferation protein #1544.
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27-NOV-2000;
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                                                                                                                                                                            Example
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                                                                                                                                                                                                                                                                                                                                         ELITRA PHARM
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                                                                                                                                                                                                                                             Ohlsen
Xu HH;
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ID ABB71
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Best Local S
Matches 136
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                  1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the printed specification, but format directly from WIPO at
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                                                                                          ABB71141
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                                26-MAR-2002
                                                                ABB71141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVTAAQQSKKVTQDEVAALVTKINNDKNNAIAEINKQTTAQGVTTEKDNGIAVLEQD--V
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                                                                                                                                                                    AQETAIDGNIG-STTEEKAAAKQQVQTEKTTADAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAG
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Pred. No. 0.00016;
4; Mismatches 275;
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   SEQ
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ALIGNMENTS

Qy 8 MESGPESVSSNOSSMNPIINGOIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALI 67	Query Match 91.9%; Score 2943; DB 16; Length 647; Best Local Similarity 93.9%; Pred. No. 7e-110; Matches 613; Conservative 15; Mismatches 19; Indels 6; Gaps 1;	SQ SEQUENCE 647 AA; 68525 MW; COD14C2D74473625 CRC64;		 RA Davis R.W.:			OC bacceria; chiamydiales; chiamydiaceae; chiamydia. OX NCBI_TaxID=813;	Chlamydia trachomatis.	CHLPN 76 kDa homolog.	01-JUN-2002 (TremBLrel.	DT U1-NOV-1998 (TEMBLICAL 08, CREATED)	084627;	ID 084627 PRELIMINARY; PRT; 647 AA.

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Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update
CHLPN 76 kDa HOMOLOG_1 (CT622).
CPN0728 OR CPU0728 OR CPU018.
CPN0728 OR CPU0728 OR CPU018.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophil
SEQUENCE FROM N.A. STRAIN=J138; MEDLINE=20330349;
                                                                                                           MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., i
White O., Hickey E.K., Peterson J., Utterback
Linher K., Weidman J., Khouri H., Craven B., i
Gwinn M., Nelson W., DeBoy R., Kolonay J., McC
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mon
                                                                                                                                                                                                                                                                                                                                     STRAIN-CWL029;

MEDLINE-99206606; PubMed-10192388;

MEDLINE-99206606; PubMed-10192388;

Kalman S., Mitchell W., Marathe R., Lammel C., Fan J.,

Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

"Comparative genomes of Chlamydia pneumoniae and C. tra
Nat. Genet. 21:385-389(1999).
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                                                                                         28:1397-1406(2000)
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y K., Bass S.,
, Dodson R.,
, Salzberg S.1
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Matches 233
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EMBL; AE001654; AAD18867.1; -.
EMBL; AE002165; AAF37914.1; -.
EMBL; AE0022547; BAA398935.1; -.
PHCI-2DPAGE; Q9Z7H7; -.
TIGR; CP0018; -.
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                                                                                          VLVNIGSLYSGYL
                                                                                                                                                                                                                                                                                                                                         QKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAFIQQ
                                                                                                                                                                          SVPRARTEARG-PEKTDQALARVISGNSRTLGDVYSQVSALQSVMQIIQSNPQANNEEIR
                                                                                                                                                                                     SVSRSGIESQGRSADASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQANQEEIM
                                                                                                                                                                                                                   GSSVKQLYKT--SKSTGSDYKTQISAGYDAYKSINDAYGRARNDATRDVINNVSTPALTR
                                                                                                                                                                                                                               QMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRS-GVQSAISQTANPALSR
                                                                                                                                                                                                                                                           K---AAGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAGVPPAAASSI
                                                                                                                                                                                                                                                                     SDQLVGADGELPAEIQAIKDALAQAL-KQPSADGLATAMGQVAFAAAKVGGGSAGTAGTV | | : : | | | | | | : : | : | : | | | | | : :
                                                                                                                                                                                                                                                                                                  LNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNI---SYEA
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                                         PRELIMINARY;
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Pred. No. 2.7e-28;
6; Mismatches 262;
                                         PRT;
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Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
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MEDLINE-94156481; PubMed=7509320;
MEDLINE-94156481; FubMed=7509320;
Perez-Melgosa M., Kuo C.-C., Campbell L.;
"Isolation and characterization of a gene pneumoniae 76-kilodalton protein containing the second 
                       Correia F.F., Allen T.W., DiRienzo J.M.; "High molecular weight serine-rich protein gene (srpA): "treptococcus crista."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; U96166; AAF34780.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9KX33;
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EMBL; L23921; AAA23117.
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                                                                                                                                                                                                                                                                                                           Streptococcus cristatus
                                                                                                                                                                                                                                   Streptococcaceae; NCBI_TaxID=45634;
                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes;
                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K---AAGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAG
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       IPR001899;
                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.) (TrEMBLrel.
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                                                                                                                                                                                                                                                         tes; Bacillus/Clostridium group; Lactobacillales;
Streptococcus.
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Query Match
Best Local Similarity
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Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus
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O8VQ99;

O1-MAR-2002 (TrEMBLrel. 20,

O1-MAR-2002 (TrEMBLrel. 20,

O1-JUN-2002 (TrEMBLrel. 21,
Sharp L.J., Henderson "Identification of a p
                                       SEQUENCE FROM N.A.
STRAIN-FRI326;
                                                                                                    Staphylococcus.
NCBI_TaxID=1280;
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O O990Y4

C O990Y4;

T 01-JUN-2001 (TrEMBLrel. 17, Created)

T 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical protein SAV2654.

GN SAV2654 OR SA2447.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699),

OS Staphylococcus aureus (strain N315).
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Best Local Sim
Matches 144;
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Pfam; PF00746; Gram_pos_anchor; 1.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

SEQUENCE 2283 AA; 228866 MW; 9C0991E0E59B24B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF450093; AAL58470.1; -.
                                                                                                                                                                                                                                                      1417
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                                                                                                                                                                                                                                                                                                                                                                                             YSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQRAAETIVRDS
                                                                                                                                                                                                                                                  TSESDSQSTSTYTSQSTSQSESTSTSTSTSDSTSISKSTSQSGSTS
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                                                                                                                                                                                                                                                                                                               TSMS--LSMSQSISGSTSTSTSTSLSDSTSTSLSLSASMNQSGVDSNSASQSASTSTSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQSGSTSTSTSTSSSVRTSESQSTSGSMSTSQSDSTSISTSFSDPTSDSKSASTASSESI 1125
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es 308; Indels 112;
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                              Bacillales;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete P
SEQUENCE 2271 AA; 227844 MW;
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NCBI_TaxID=158878,
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                      SVSDSTSDSTSASTSGSMSVSISLSDSTSTSTSASEVMSASISDSQSMSESVNDSESVSE
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                                                                    -STSASGSASTSTSTSD--
                                                                                           YSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQ-----RAAETIVRDSQTLGD
                                                                                                                                          AMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSL
                                                                                                                                                               TSTSLSNSASASE---SDSSSTSLSDSTSASMQSSESDSQSTSASLSDSLSTSTSNRMST
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                                                                                                                    ----IASLSTSVSTSESGS-----TSESTSESDSTSTSLSDSQSTSR----
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20.6%; Pred. No. 0.011;
                                                                     -SRSTSASTSTSMRTSTSDSQSMSLSTSTSTSMSDSTSLSD
                                     RLQVLDS-------LMSTIVSNPQANQEEIMQKLTASI
-ADSLQKFAAQLEREFVDGERSLAES
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Best Local Similarity
Matches 150; Conserv
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Q99U54;
Q99U54;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
     6009
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EMBL; AP003133; BAB42527.1; -.
Complete proteome.
SEQUENCE 6713 AA; 722339 MW
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EbhA protein.
EBHA OR SA1267.
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                                                           428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLN-----KLV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDAILNKNSSPTDSLSQL---EASTSTSTVTRVAAKDYDEAKSNFDTAKSGLENAKTLAE
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                                                     DALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSY
                                                                                                             MTKEETEQAKAQLAQALKETKDLVKAKENAKQDVDKQVQALTDETDQNPNLTDKEKQALK
                                                                                                                                                                        ATAKELQAMEAQLT - - -
                                                                                                                                                                                                                                                                                SAASAGSAAGALKSSNNSGRISLLLDDVDN--EMAAIALQGFRSMIEQF-----NVNNP 392
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48	NHATEQVHANETPKAKIDANKDVDKQVQALIDETDRNPNLTDK 58	5806	Db	
4	SQAAVLQAQQNNSPDNIAATKE 28 ;	225	Qy	
805		5746	Db	
24	TLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQ- 2	179	Qy	
745	RLANTLINSDNT-NVNDINGAIQAVNDAIHNINGDQRLQDAKDK 5	5703	рь	
8	YETKMADLMAALQDMERLANSDPSNNHTE	127	Qy	
702		5664	Db	
ō	RDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKD	70	Qy	
663	NGDQNLANAKDKANAFVNSLNGLNQQQQDLAHKAINNADTVSDVTDIVNNQIDL 5	5610	Db	
-	SGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAK	10	Qy	
31;	y Match 8.1%; Score 261; DB 16; Length 6713; Local Similarity 20.5%; Pred. No. 0.078; hes 150; Conservative 133; Mismatches 237; Indels 210; Gaps	Query M Best Lo Matches	X W O	
	ENCE 6713 AA; 722306 MW; BBCC0536AC341BF5 CRC64;	SEQU	SQ	
	; AP003362; BAB57596.1;	EMBL	DR	
	aureus."; Lancet 357:1225-1240(2001).	Lanc	P 전	
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-	tuhara S., Goto S., Yabuzaki J.,	Seki		
	I.K., Sawano T., In	Mizu		
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	na I., Baba T., Yuzawa H.,	Kuro	RA	
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36	QKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENA 6	587	Qy	
155	LQNVENAQTIDQLNRGLNLGLDDIRNTHVWEVDEQPAVNEIFEATPEQILVNGELIVHRD 6	6096	ф	
86	ETIVRDSOTLGDVYSRLQV-LDSLMSTIVSNPQANQEEIM	548	Qу	
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EMBL; AF350283; AAK30612.1; -. NOW_TER
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Fibroin 3 (Fragment).
Plectreurys tristis (Spider).
Eukaryota: Metazoa; Arthropoda; Chelicerata; Arachnida; Araneomorphae; Haplogynae; Plectreuridae; Plectreurys.
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01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 27,
01-JUN-2002 (TrEMBLrel. 21,
Putative transglycosylase.
                                                                                                                                               InterPro; IPR002886; Peptidase_M37.
InterPro; IPR002189; SLT_domain.
Pfam; PF01551; Peptidase_M37; 1.
Pfam; PF01464; SLT; 1.
PROSITE; PS00922; TRANSGLYCOSYLASE; 1.
PROSITE; PS00922; TRANSGLYCOSYLASE; 1.
SEQUENCE 2285 AA; 252310 MW; FF602C227754B357 CRC64;
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Karamata D.;
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                                        SAIDTYQKNLKSYNQTVKETSTVIKNADGSVEKLTQQYKKNGEILQRETKIINN-----
                                                                    SGPESVSSNQSSMNPII---NGQIASNSE-----TKESTKASEASPSASSSVSSWSFLSS
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O1-JAN-1998 (TrEMBLrel. 0
O1-JAN-1998 (TrEMBLrel. 0
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YOMI protein.
MEDLINE-98044033; PubMed-9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessiteres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
                                                                                                                                                           Bacillaceae;
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Bacteria; Firmicutes;
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RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gulseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Gulseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Liardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medique C.,
RA Hedina N., Mellado R.P., Mizumo M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic C., Pornelle B., Rapport G., Rey M., Reynolds S.,
RA Presecan E., Pujic C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
"The complete genome sequence of the gram-positive bacterium Bacillus RT subtilis ":
"The complete genome sequence of the gram-positive bacterium Bacillus
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Submitted (NOV-1997) to the
EMBL; Z99115; CAB14053.1; -
HSSP; P00718; 153L.
InterPro; IPR002886; Peptid
InterPro; IPR000189; SLT_do
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InterPro; IPR000189; SLT_domain.
Pfam; PF01551; Peptidase_M37; 1.
Pfam; PF01464; SLT; 1.
PROSITE; PS00922; TRANSGLYCOSYLASE;
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19.3%; Pred. No. 0
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   - NVSDLTPDDTVNTLTAAMLNF
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Complete proteome.
SEQUENCE 1063 AA; 104547 NO.
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BEOLOTIA A., Wincker P., Mauger S., Jaillon O., Malarme
Belottin A., Wincker P., Mauger S., Jaillon O., Malarme
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacter
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL; AE006319; AAX04950.1;
InterPro; IPR001899; Gram_pos_anchor.
PRINTS; PR01608; BACINVASINC.
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ST--VGISGLANIFSTLGTFNIPGMTTAAAALNGVEQIVNI---
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                                                     SNFDTAKSGLENA-KTLAEYETK-MADLMAALQDMERLANSDPSNNHTEEVNNIKKALEA
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01-JUN-2001
01-DEC-2001
                                                                                                                                                 Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an MI strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                   Streptococcaceae;
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein SPy0697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AONO;
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                                                                                                                      Hypothetical SEQUENCE 10
                                                                                                                                                                                                                                                           STRAIN-SF370 / ATCC 700294 / SEROTYPE MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDLDTLVSLQGNDLVNYLAGLVVNSAINRV-GQIAWSQ-----LSPTISNIPLVGTTVNN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELIDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSG--
                              SVSSNQSSMNPIINGQIASNSETKES-----TKASEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSLNSFGNLPAGASDILNQVLNQLQNAINNIVESATGIVNNLPG-LGAIENGLSNTISQI 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLSPTLNNLTGASLGEVA-----NLTGVSSLLDQVNNSLGNLISLGSTALATIENTLQ 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYEAVLT--NAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNI--AAT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AANPGAFLLNEIKS----
SMSIGATTIKTVTAVQAVSTTMTKADMVARLSQLGVLKASTVIYGVMTGAISLSTAATIA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSSESSASSSNSSEGSVASSSSVDSSQSSSAGVNSSSSSAEGSSASSSNSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSAGVNSSSSSAEGSSASSSNSSESSVASSSS-----
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                                                                          Similarity
                                                                                                                      il protein;
1086 AA; 1
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(TremBLrel. 17, Last sequence update)
(TremBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NNPATAKE-----LQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQ- 436
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                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                 pyogenes
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                                                                          7.3%;
21.4%;
                                                                                                                      115601 MW; 87592EE
                                                            116;
                                                                          Score 233;
Pred. No. 0.
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                                                            Mismatches
                                                                                                                      87592EB52CDD5ADB
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                                                                                        Length 1086;
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                               ----SPSASSSVS
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Q49545;
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01-NOV-1996 (TIEMBLIEL C
01-DEC-2001 (TIEMBLIEL C
                                                                                                                                      LMP1
                                                                                                              Mycoplasma hominis:
Bacteria; Firmicutes;
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Christiansen G.;
"A 135-kilodalton surface antigen of Mycoplasma
                        MEDLINE-95104998; PubMed-7806360; Ladefoged S.A., Birkelund S., Hau
                                                   STRAIN-PG21
                                                              SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=2098;
                                                                                                 Mycoplasmataceae;
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Last sequence update)
Last annotation update)
                         Hauge S.,
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                         Brock B.,
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  hominis PG21 contains
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RESULT Q49525
ID Q49525
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EMBL; X81475; CAA57228.1;
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Bacteria; Firmicutes; Bacillu Mycoplasmataceae; Mycoplasma

Bacillus/Clostridium

group; Mollicutes;

Mycoplasma hominis.

LMP1. Lmp1.

SEQUENCE FROM

N.A.

NCBI_TaxID=2098;

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RESULT
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EMBL; U21962; AAA81013.1; -
  Bacteria;
                          Streptococcus gordonii.
                                                                                                                                                                                 Q9KWR3;
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MEDLINE=95369882; PubMed=7543881;
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Bacillus/Clostridium
                                                                                                Last sequence update)
Last annotation update)
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Best Local Similarity
Matches 145; Conserv
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Takahashi Y., Konishi K., Yoshikawa M.;
Takahashi Y., Konishi K., Yoshikawa M.;
"Cloning and characterization of the gene encoding a hen
Streptococcus gordonii DL1.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AB029393; BAA97453.1; ...
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NCBI_TaxID=1302;
[1]
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InterPro; IPR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 2178 AA; 203507 MW; 75CC27E27F41DA8C CRC64;
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 TSASVSASE
                                                           SASVSASTYASTSASVSASES
                                                                                        TIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQANQEEIMQKLTASISKAPQFGYPAVQNSA
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19.9%;
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Best Local S
Matches 165
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Katsukawa C., Fujinaga Y., Abe Y., Watanabe H.;
"Complete sequence of temperate phage phiniHill.",
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYOS0245; AALI5083.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcaceae; NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tail protein.
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                                                                                                                                   KVGGGSAGTAGTVQMNVKQLYKTAFSSTSSS----SYAAALSDGYS-----AYKTL
                                                                                                                                                              VLDSAGVEMPEKVKGMVTNVSTGLQAELQAANFAQLGQEIPNGVSQGISQGAGKASDASV
                                                                                                                                                                                       QLVGADGELP------AEIQAIKDA-LAQALKQPSADGLATAMGQVAFAAA 454
                                                                                                                                                                                                                                             NNSG-----RISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSD
                                                                                                                                                                                                                                                                                       HTGLTDSPLVKKAEEQISQAQKDIQEIKPS----GSDIPIVGPSGSAASAGSAAGALKSS
                                                                                                                                                                                                                                                                                                                            TQLQEEYNKTSATQQAAADAMAAAEESGSARQVIAYENMSEAQRTAIDNMRTKYSELLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKQLR-----DSVREGVQERKKGLESVKESTAAHQKLADEIIKLAAKE-----NKT
AAQSIAARITATIQSALDIHSPSRVMRDEVGRFI--PQGIAVGIDADRKVIDSSMQKLKE
                        ASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQ------ANQEEI---MQKLTA 591
                                                                                                          KMG-------QEVKRSFQGELGIHSPSRVFTEYGGHITDGLSNGVTNGTSKVMQTM
                                                                                                                                                                                                                     RRMGPEGATQTQVFVDATDAELAPLQ-ENFRAATE----TAK----NAMGS
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Last sequence update)
Last annotation update)
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                                                     ITDAFSTMSGPMHSHGVNAMQGLANGIYAGSGAALA
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                                                                      -SAISQTANPALSRSVS----RSGI-ESQGRSAD
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Best Local
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Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY028381; AAL13053.1; -.
EMBL; AY028381; CAML3053.1; -.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 3072 AA; 285770 MW; 0B148372697CF7F2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Platelet binding protein GspB.
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132; Conserv
GTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPAL
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                                                                                                                                                                                                ASVSANESASTSASVSASESASTSASVSASESASTSASVSASESASTS
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Pred. No. 0.61;
27; Mismatches
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.61;
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Best Local S
Matches 137
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J. Antimicrob. Chemother, 45:421-431(2000).
EMBL; AB025716; BAA93438.1; -.
TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
TIGRFAMS; TIGR01168; YSIRK_signal; 1.
SEQUENCE 2478 AA; 262995 MW; 1C118EBE0DB03B34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20348625; PubMed=10896508; Komatsuzawa H., Ohta K., Sugai M., Fujiwara T., Glanz Komatsuzawa H.; Suginaka H.; Berger-Bachi B., Suginaka H.; "Tn551-mediated insertional inactivation of the fmtB "Tn551-mediated protein abolishes methicillin rectal wall-associated protein abolishes
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TAMSDQLVGADGEL-PAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGTA
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                                          -----NEEISKIENITDSTQTKMDA-----YNEVKQAATARKAQNATAS-
                                                                                                               DAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAG
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Pred. No. 0.
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Best Local S
Matches 152
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Povoa M., Barnwell J.W.;
"Plasmodium vivax merozoite surface proteins-3beta and-3gamma structural similarities with P. vivax merozoite surface protei and define a new gene family.";
Mol. Biochem. Parasitol. 115:41-53(2001).
EMBL, AF099663; AAF78288.1;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
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                                                                                                LFVTKAMAAKEKAKKSAEAADKAKA---QAEAVNGASE--KTKKDAEHAATKANE-KKTH
                                                                                                                                                                                               EVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIK 248
                                                                                                                                                                                                                                                               LMAALQDMERLANSDPSNNHTEEVNNIKKA-----LEAQKDTIDKLNKLVTLQNQNKSLT 188
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   SGR I SLLLLDDVDNEMAA I ALQGFRSM I EQFNVNNPATAKELQAMEAQLTAMSDQLVGADG
                                TETAADAAKKNAEVKVEEEDNVAKNEEKMKKKVDDV-----IEKVLEALKSEED
                                                      TGLTDSPLVKKAE---EQISQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSSNN
                                                                                                                              L-----GQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEH
                                                                                                                                                                EATKPSSKAANV-----KKKTDEAIK------AAKEAKKAKTEAYIA 443
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Q9LCJ9;
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f 01-OCT-2000 (TrEMBLrel. 1'
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell wall-associated protein abolishes methicillin Staphylococcus aureus ; J. Antimicrob. Chemother. 45:421-431(2000). EMBL; AB015223; BAA93430.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20348625; PubMed=10896508;
Komatsuzawa H., Ohta K., Sugai M., Fujiwara T.,
Berger-Bachi B., Suginaka H.;
"Tn551-mediated insertional inactivation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000890; Acetate_kin.
TIGRRAMS; TIGR01168; YSIRK_Signal; 1.
PROSTTE; PS01075; ACETATE_KINASE_1; UNKNOWN_1.
SEQUENCE 1795 AA; 191008 MW; 6CB77CCFCB33D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
    682
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                             LTEVLKTTDSADQIPAI------NSQLEINKNSAD------QIIKDLE--RQNI 226
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                                                                                                                                           LMAALQDMERLANSDP-----SUNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQNKS
                                                                                                                                                                                                                                          LNKNSSPTDSLSQLEASTSTVTRVAAKDYDEAKSNFDTAKSGLENAKTLAEYETKMAD 133
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ITPTVKPQAKQDIIQAVTTRKQQIKKSNASLQDEKDVANDKIGKIETKAIKDIDAATTNA
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132; Conserv
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19.18;
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Pred. No. 0.38;
9; Mismatches 268
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1089
                                                                                                                                                                                                                          J. Bacteriol. 178:2775-2784(1996).
EMBL; X95601; CAA64858.1; -.
                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma hominis.
Bacteria; Firmicutes; Bacillus/Clostridium
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                            STRAIN-PG21
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                -ERLANSDPSNNHTEEVN-NIKKALEAQKDTIDKLNKLYTLQNQNKSLTEVLKTTDSA--
                                                                    ASTSTSTVTRVAAKDY--DEAKS--NFDTAKSGLENAKTLAEYET---KMADLMAALQDM 141
                                                                                                                                                           150;
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                                                                                                                                                           Conservative
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Best Local Sim
Matches 148;
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QBRJN9;
(01-JUN-2002 (TrEMBLrel. 21, Cr.
1 01-JUN-2002 (TrEMBLrel. 21, La
)T 01-JUN-2002 (TrEMBLrel. 21, La
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)T 01-JUN-2002 (TrEMBLrel. 21, La)
                                                                                                                                                                                                                                                                                                                          Signal.
SIGNAL
                                                                                                                                                                                                                                                                               CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma hominis.
                                                                                                                                                                                                                                                                                                                                                                     "Gene and Protein Structure of the Mycoplasma hominis Vaa adhesin."; Thesis (2001), Department of Department of Medical Microbiology and. EMBL; AJ416752; CAC95143.1; -.
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                                                                                                                                                                                                         Local Similarity
KTNESKVLDNSKIDENSSIEDIQNKTQEIEKAIESLTKKINDKNKKHEEDQKIVQAMQEF
                                                                                      SISLIAAAASTAAIASVCASKNNKFRKQRKYNKETEKQEINQAKENLKKLLELIKSSDID
                                                                                                                                    SLSQLEASTSTSTVTRVAA----KDYDEAKSNFDTAKSGL---
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AA; 160137 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor
                                                                                                                                                                                 Score 225; DB Pred. No. 0.3; 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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VARIABLE MEMBRANE PRO
MW; 2C03F666B3473CAB
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Query Match
Best Local S
Matches 155
                                               Bloecker H., Brandt P.;
Submitted (JUL-1996) to the EMBL/
EMBL; Z74106; CAA98621.; -.
EMBL; Z74105; CAA98620.1; -.
SGD; S0002216; USO1.
InterPro; IPR002017; Spectrin.
SEQUENCE 1790 AA; 206450 MW;
                                                                                                                                                                                                        007380; P89892;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update
Hypothetical 206.5 kDa protein YDL058W.
                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomycetas; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                                                                      SEQUENCE FROM N.A.
Bloecker H., Brand
                                                                                                                                                            Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                     Q07380
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                                                                                                                                                                                                                                                                                                                                                                        SLAESQ
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                                                                                                                                                                                                                                                                                                                                                                                                                      ----STIVSNPQANQEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGER
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEVKNKLDKFSNEKEAEFNKLEASRSAIKEFINENNTNPNYTALIQKLQAKLDAKNSITK
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              Similarity
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 Conservative
                                                                                                                                                                                                                                                                                     PRELIMINARY;
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            7.0%;
  130;
Score 224.5; |
Pred. No. 0.43
30; Mismatches
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O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CTORF1365, partial (Fragment).
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillus/Clostridium group; B
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 Wu S., de Lencastre H.;
"Mrp-a new auxiliary gene essential for optimal expression methicilin resistance in Staphylococcus aureus.";
Microb. Drug Resist. 5:9-18(1999).
                                                                                     Staphylococcus.
NCBI_TaxID=1280;
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                                          MEDLINE-99265121; PubMed-10332717;
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Q9RL69; 01-MAY-2000 01-MAY-2000 01-JUN-2002

0 (TrEMBLrel. 13, 0 (TrEMBLrel. 13, 2) (TrEMBLrel. 21,

Created)
Last sequence update)
Last annotation update)

Mrp protein

Q9RL69

PRELIMINARY;

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Bacteria; Firmicutes; Staphylococcus.

Bacillus/Clostridium

group; Bacillales;

SEQUENCE FROM N.A NCBI_TaxID=1280;

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AQETAIDGNNG-STTEEKAAAKQQVQTEKTTADAA 1076
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MEDLINE-97302526; PubMed-9158773;

Wu S., de Lencastre H., Sali A., Tomasz A.;

"A phosphoglucomutase-like gene essential f
of methicillin resistance in Staphylococcus
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"Mrp-a new auxiliary gene essential for omethicillin resistance in Staphylococcus Microb. Drug Resist. 5:9-18(1999).
EMBL; Y09927; CAB55329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which results in reduced methicillin phosphoglucosamine mutase.";
J. Bacteriol. 179:5321-5325(1997).
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"The femR315 gene from Staphylococcus
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Submitted (AUG-1997) to the
EMBL; AF019980; AAB70839.1;
NON_TER 924 924
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NCBI_TaxID=44689;
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21.1%;
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Pred. No. 0.25
22; Mismatches
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Last sequence update)
Last annotation updat
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Q902QO

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Q11001

Q11001

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Best Local S
Matches 152
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Axoneme-associated protein GASP-180.
Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50088; ANK_REPEAT; 2.
PROSITE; PS50297; ANK_REP_REGION; 2.
PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
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Submitted (JUL-2001) to the EM
EMBL; AF400249; AAK91740.1; -.
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01-DEC-2001
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Interpro; IPR000194; ATPase_a/bcentre.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAI----NSQL---
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                ARDNQIAEL - - - - KELVD - - -
                                                               -- DNEMAATALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAI
                                                                                                                                                                   KKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDV-
                                                                                                                                                                                                                        ANAKQDIDERDDEIE--LLRDRIQEEMKNSAALQERVDALE-----ADATRG
                                                                                                                                                                                                                                                                            GQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLV
                                                                                                                                                                                                                                                                                                                                 QDLVMRAESAQRSSAEGDKRVAQLEAQIAGLERLLADAQGGDDERVKELNEQIADLQFEL
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Associated Proteins in Giardia lamblia.";
2001) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 0.5
                -GAPAQPVEADPAQLTALEEE----
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CG18304 OR CG13774.
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BMBL, AE003615; AAF52458.2; -
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                                                                                                                                                                                                                                                                                                                     GERSLAESQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALSRSVSRSGIE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVATVQSDM----STSVENLVTSNVAVTQTD----FEVPDRNVSIERETMSSPFAGLFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPA-TAKELQAME
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                                                                                                                                                                                                                                                                                                                                                                       KVEDLEKENAESKKYV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSSSRVGQSGRKLSPTPHPHRLAPEVHADRDEGIS-DEDDPAELRILLELNEQEASILRL
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145; Conserv
histolytica
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21.6%; Pred. No. 0.7;
tive 105; Mismatches
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Last sequence up
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Best Local
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Pfam; PF00613; myosin_head; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMARP; SM00242; MYSC; 1.
SMARP; SM00242; MYSC; 1.
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1543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raymond-Denise A., Sansonetti P., Guillen N.; "Identification and characterization of a myosin heavy chain gene (mhcA) from the human parasitic pathogen Entamoeba histolytica."; Mol. Biochem. Parasitol. 59:123-131(1993).
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NCBI_TaxID=5759;
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SELEEQVNELESRPYGTG
                          SAISQTANPALSRSVSRSGIESQGRSADASQRAAETIVRDSQTLGDVYSRLQVLDSLMST
                                                                          AGTAGTVQMNVKQLYKTA---
                                                                                                                 KEKQVKKLEGELKETKDKLNAAI-AEKDSIFTAKKQSDAD---
                                                                                                                                           MEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGS
                                                                                                                                                                        QRDKLVADNKKMTKTLEEIKARDEENTYKVENYEKVLKRKEADLEEANENLDIEKKDRMN
                                                                                                                                                                                                     GRISLLLD----
                                                                                                                                                                                                                              ESKNKDSENEKAALSEEIDQANEKLKNIQ---ADL----RKATADLQEANEKKAEVEA
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                                                        LEELNKTVEEHDEVVAKLNTQITKLTRDNQSAEEELNELRSKADKDKKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.9%;
20.9%;
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                                                                                  -FSSTSSSYAAALSDGYSAYKTLNSLYSESRSGVQ--
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Pred. No. 0.
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EIKIRDAQ-IADLNKALE
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EMBL; AY07
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Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Eukaryota; Metazoa; Arthropoda; Trac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             LKTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIKLG
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QESSSS----
                                        QLTAMSDQLVGADGELPAE------IQAIKDALAQALKQPSADGLATAMGQVAFAA
                                                                                                                                                                                                                                                    KAEEQISQ------AQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSS------
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                                                                                                                                                                                                   EPSTEANESSSTESSQDSTTQESSSSSEGPLSTESSTEANESSSTESSQDSTTQESSSST
                                                                                                                                                                                                                                                                                                         SSTESSQDSTTQKSSSSTESPLSTEPSTEANES - - - SSTESSQDSTTQESSSSTEGPLST
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AY075323; AAL68190.1; -.
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-SEGPLSTESSTEANESSSTESSQDSTTQESSSSTEDPLST-----
                                                                                                                                                NNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEA
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Endopterygota; Diptera; Brachycera; Musc
ilidae; Drosophila.
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Best Local Similarity
Matches 140; Conserv
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Q9ZFF9;
01-MAY-1999 (TrEMBLrel. 10, Li
01-MAY-1999 (TrEMBLrel: 21, Li
01-JUN-2002 (TrEMBLrel: 21, Li
Fimbriae-associated protein Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu H., Fives-Taylor P.M.;

"Identification of dipeptide repeats and a cell wall sorting the fimbriae-associated adhesin, fapl, of Streptococcus paras Mol. Microbiol. 34:1070-1081(1999).

EMBL; AF100426; AAC79868.1; -.

InterPro; IPR001899; Gram_pos_anchor.

InterPro; IPR001313; Pumillo/Puf.

Pfam; PF00746; Gram_pos_anchor; 1.

PGAM; TIGR01167; LPXTG_anchor; 1.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

SEQUENCE 2570 AA; 263107 MW; B90E035675A409A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcaceae; Streptococcus.
NCBI_TaxID=1318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus parasanguis.
Bacteria; Firmlcutes; Bacillus/Clostridium group; Lactobacillales;
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                                                 ELKQEHTGLTDSPLVKKAEEQIS---QAQKDIQEIKPSGSDI-----PIVGPSGSAA--
                                                                                                     ----RSTTTGTKTTFTISDFSNGGTQYYWA--GGNANNLKNPISSISAVYDSATGKISW
                                                                                                                                                       GEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAETKVN-
                                                                                                                                                                                                              NLIGDPNATVADLQIAYTTLGNNTQALGNELIKLNPNG--QIYAVLNNTEASRAATL---
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19.7%; Pred. No. 1.2;
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                                                                                                                                                                                                                       Complete proteome. SEQUENCE 4776 AF
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EMBL; AE007470; AAK75846.1;
TIGR; SP1772; -.
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Streptococcaceae; Stre
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PF00746; Gram_pos_anchor; 1.
PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
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SMART;
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01-NOV-1998 (TrEMBLrel. 28, Last sequence u
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Myosin heavy chain isoform A.
Loligo pealeli (Longfin squid).
Eukaryota, Metazoa; Mollusca; Cephalopoda;
Myopsida; Loliginidae; Loligo.
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Pfam;
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                                                                                                                                                                                          InterPro;
InterPro;
                                                                                                                                                                                                                                                                                            Matulef K., Sirokman K., Perreault-Micale C.L., S "Amino-acid sequence of squid myosin heavy chain. J. Muscle Res. Cell Motil. 19:0-0(1998). EMBL; AF042349; AAC24207.1; -. HSSP; P24733; IWDC.
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TISSUE-VENTRAL SIPHON MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myopsida; Loliginidae;
NCBI_TaxID=6621;
                                             SMART;
                                                            PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                               InterPro;
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  ; SM00353; HLH; 1.
; SM00015; IQ; 1.
; SM00242; MYSC; 1
                                                                                                        PF00063; myosin_head;
PF02736; Myosin_N; 1.
PF01576; Myosin_tail;
                                                                                                                                                                     PF00612;
                                                                                                                                                                                    IPR001609; myosin_head.
IPR004009; myosin_N.
IPR002928; myosin_tail.
                                                                                                                                                                                                                                                       IPR000048; IQ_region
                                                                                                                                                                                                                                                                         IPR001092; HLH_basic
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                                                                                                                                                                       ĮQ;
                                                                                                   Myosin_tail; 1.,
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Last sequence update)
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RESULT 35

Q9HGK
ID Q9HGK
AC Q9HGK
AC Q9HGK
AC Q9HGK
DT 01-M2
DT 01-DE
A991u
GN ALS7
OS Canddi
OC Eukar
OC Sacct
OX N(CB1_1
RN [1]
RN [1]
RY MEDLI
RX MEDLI

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                                                                                                                                                               Q9HGK6 PRELIMINARY; PRT; 2297 AA.
Q9HGK6; PRELIMINARY; PRT; 2297 AA.
Q9HGK6; PRELIMINARY; PRT; 2297 AA.
Q19HGK6
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Apglutinin-like protein Als7p.
ALS7.
                                                                                                 Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
SEQUENCE
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  MEDLINE-20321177; PubMed-10861907;
                       SEQUENCE FROM N.A.
STRAIN-1161;
                                                                              NCBI_TaxID=5476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                QFGYPAVQNSADSLQKFAAQLERE-----FVDGERSLAESQENAFRKQPAF
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                                                                                                                                                                                                                                                                                                                                                                                         Q-----TADTLHSKCAGLEKAKSRLQGELEDLAIDVERSSAHA-NNLEKKQRNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKIDDQARSVSELTSQKSRLQTEAADLTRQLEEAEHNVGQLTKL-----KSSLGASLED 1313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DGLATAMGQVAFAAAKVGGGSAGTAGTV---QMNVKQLYKTAFSSTSSSSYAAALSD 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NELGDQIDQLQKVKSRLEKEKTQLRAEMDDVQSQVEHAGKNRGCSEKMSKQMEAQLSELN
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1935 AA; 221530 MW;
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Pred. No. 0.94;
                                                                                                   Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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Best Local
085472
085472;
01-NOV-1998
01-NOV-1998
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(TrEMBLrel.
                                                             PRELIMINARY;
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HOYER L.L., Hecht J.E.;
"The ALS6 and ALS7 genes of Candida
Yeast 16:847-855(2000).
EMBL; AF201684; AAF98068.1; ...
SEQUENCE 2297 AA; 244723 MW; 59B
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nes 146; Conserv
                                                                  -- QNSADSLQKFAAQLEREFVDGERS-LAESQENA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSSIPIMSSSDESSESRESSSGTILSEENSDSIPTTFSTRYWSPSGMSSRHYTNSTETSV 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSVISESSESVTSESVASESVASESVTAVSDISDLYTTSEVVSTSDSKIVPSTSVPSSEQ 1653
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SGSSSADHQSSATCDVSESSVEGNLSAMAPGMSNS
                                                                                                                                                                                                    RLQVLDSL----MSTIVSNP-----QANQEEIMQKLTASISKAPQFGYPAV-----
                                                                                                                                                                                                                                                                       SEVVSTSDSNSGMSPPIPSSEQRSSIPVMSSSNESSESRESSSGTILSEENSDSIPTTFS
                                                                                                                                                                                                                                                                                                          SRSGVQSAISQTANPALSRSVSRSGI---ESQGRSADASQRAAETIV--RDSQTLGDVYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESSSGTILSEENSDSIPTTFSTRYWSPSGMSSRHYTNSTETSVSDVVSSSVAGDETSESS 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVNELKQEHT-----GLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSG-SAASA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETSVSDVVSSSVAGDETSESSVSVISESSESVTSESVASESVAS-----ESVT
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                                                                                                                                     TRYVSVSLTVGELSALPSLPGKLSHLPSSLSETSIGMTKSANLSPQFFSTSVDSALSYWA
                                                                                                                                                                                                                                                                                                                                                                                                            SDVVSSSVAGDETSESSVSVTSESSESVTSESVASESVASESVASESVTAVSDISDLYTT 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYA--AALSDGYSAYKTLNSLYSE 507
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"Characterization of emb, a gene enco
Streptococcus defectivus";
Infect. Inmun. 67:50-56(1999).
EMBL; AF067776; AAD03320.1;
-TIGREAMS; TIGRO1168; YSIRK_signal; 1.
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SEQUENCE 2055 AA; 215642 MW; 9699
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                                     AKKAAI--TANNALTQEEKAAAIKQVEDEAAKAQAAVDASRSKADVDRAKDQGLQKISDV
                                                                             GVQSAISQTANPALSRSVSRSGI----ESQGRSA----DASQRAAET-IVRDS--QTLGDV
                                                                                                                                                            --AKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGY-SAYKTLNSLYSESRS
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YSRLQVLDSLMS--
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-TIVSN----PQANQEEIMQKL---
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Pred. No. 1.
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STRAIN-MARFER03099;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Kimura T., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Shimpo S., Sugimoto M. Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;

Takeuchi C., Yamada M., Tabata S.;
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DNA Res. 7:331-338(2000).
EMBL; AP002995; BAB48310.1;
Complete proteome.
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
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                                                                       SPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIP 334
                                                                                                                                                                           T-----LAAMIDQGK--TQI--GADMADIVTSTSSMLEARASDFAGRMEAARHVVSRSF
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-----ASLGSHLERLEEGRN--RLSLAL----
                          IVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQF---NVNN
                                                       --EKFAESRDGIDAAVT--NQVQKLAEGRS---LIARALEE-
                                                                                                                  DSDIQRLADARVGIEEAVENHSRKLSESRD----
                                                                                                                                            DQIIKDLERQNISYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNN
                                                                                                                                                                                                                                      AERGQALISEFQTRAEALDTGTQKLNAALEARARQIN----ETLVERAREIAHTFAESKD
                                                                                                                                                                                                                                                                   AE-----YETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKD 169
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"Selection of Mycoplasma hominis PG21 deletion mutants
in the presence of morelonal antibody 552.";
Infect. Immun. 63:3336-3347(1995).
EMBL; U21963; AAA81014.1; -.
SEQUENCE 716 AA; 79864 MW; 28D08C3EOC91CB47 CRC64;
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NCBI_TaxID=2098;
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Bacteria; Firmicutes; Bacillus/Clostridium
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                         GALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQF---NVNNPATAKELQAMEAQLT 406
                                                                                                                                                                                                                                                                                                                                                                                       NQLLPQ----LSDNDSETAKAKKSLDAEIKNANQAVASNNTASMQSAKSSLDAKVAEITK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLESTLIEIQNATNNLIKLLNESTKEKDNIDNLNAK-------EQLKASISQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SADSLQKFAAQLEREFVDG----ERSLAESQENAFRKQPAFIQQVLVNIASLFS
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SSLDAKVAEITKKLETFNKDKEAKFNELKQTRNQIQEFINTNKNNP----NYSELISQLT
                                                                                                                                          ETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAA
                                                                                                                                                                                          DSSNKSDIESANTELKQALAKANADKVQADNLAKS--IKEQLNNSVSNANTLSAKLTD--
                                                                                                                                                                                                                                       --TNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNI-AATKELIDAA
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EMBL; AE006392; AAKOS715.1; -
PRINTS; PR01608; BACINVASINC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcaceae; NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown protein.
YQFG OR LL1617.
                                                                                                                                                                                                                                                                                                                              SEQUENCE 1072 A
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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 QSQAAVLQ----AQQNNSPDNIAATKELIDAAETKVNE-----LKQEHTGLTDSPLVKKA
                         SGSDNLTKDSSEISTSGAFLSSNQTSSEA-STNSNSSI-SLSPSNISSTSVLESTTSSSN
                                                  NSADQIIKD
                                                                         SSTSDSESATNSSDFSNVAEVANNSLASVNNSSSS---VLSSTSTAD-----
                                                                                                                          SNEESEHSNSSNINETNNSSEITNILPPSNPTESNSVSDQTSSEASTNSNSSISLSPSNI
                                                                                                                                                  DMERLANSDPSN----NHTEEVNNI-------
                                                                                                                                                                            LDSSISSSQTENSQSGASSTAEISYDSENSN-SLSSSNQINSNSNSEKDSNQSSLGSSMS
                                                                                                                                                                                                                             SSSNSVEQVDVASSESTQDANSASLYPISEASSVT
                                                                                                                                                                                                                                                     SSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRDAILNKNSS
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                                                                                                                                                                                                    PTDSLSQLEASTSTYTRVAAKDYDEAKSNFDTAKSGLENAKTLAEYETKMADLMAALQ
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                                                                                                                                                                                                                                                                              Conservative
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19.7%;
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                                                -LERONISYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAGD
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Pred. No. 0.
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Last annotation updat
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RESULT 40
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Best Local S
Matches 141
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                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8T8Q5;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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381 LINTLKESYAIKEQQVVTLEAQLEA-----IRVENEQKVKDLQKQNEDRNTQASDSSE
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                                                                    HTELELKDTEVRKLQEKLKQLESQRESHNNEVKEQFKKLQATKQEVDAK-----LMATEH 380
                                                                                                       HHHMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKN 64
                                                                                                                                                                                                              AY075577;
ENCE 1489
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                                                                                                                                       6.6%; Scilarity 19.1%; Pr
Conservative 127;
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                                                                                                                                                                                                              AAL68382.1; -. AA; 170145 MW; 876DC2DE469945AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                      Score 213; DB 5; Length 1489;
Pred. No. 0.98;
77; Mismatches 288; Indels 18
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123 TIAEYETKMADLMAALQDMERLANS
71 4 19 19 19 19 19 19 19 19 19 19 19 19 19

Search completed: March 12, 2003, 12:21:40 Job time: 133 secs

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

on: March 12, 2003, 09:42:47; Search time 21 Seconds

(without alignments)
1303.542 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-007-693-139 3204 1 MHHHHHHMESGPESVSSNQS......PAFIQQVLVNIASLFSGYLS 660

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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EMBL; X54378; CAA38253.1; -.
EMBL; L03188; AAB00143.1; -.
EMBL; U53668; AAB66659.1; -.
PIR; A38455; A38455.
SGD; S0002216; USO1.
InterPro; IPR002017; Spectrin.
Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.

5	44	43	42	41	40	39	38	37	36	S	34
183.5	183.5	183.5	183.5	184	184	184	185.5	185.5	185.5	185.5	186
5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.8	5. 8	5.8	5.8	5.8
1976	1935	1561	1208	1976	1939	881	1947	1427	1205	1087	1972
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MYHA_BOVIN	MYH7_RAT	SPAP_STRMU	PCP1_SCHPO	MYHA_HUMAN	MYH4_HUMAN	YJH8_YEAST	MYSC_CAEEL	REST_HUMAN	SMC_MYCTU	AKA9_RABIT	MYHB_HUMAN
	P02564 rattus norv										

ALIGNMENTS

DILEAST STANDARD; PRT; 1790 AA. P25386; 01-MAY-1992 (Rel. 22, Created) 01-MAY-1992 (Rel. 22, Last sequence update) 16-CCT-2001 (Rel. 40, Last sequence update) 17-CCT-2001 (Rel. 40, Last sequence update) 18-CCT-2001 (Rel. 40, Last sequence update) 19-CCT-2001 (Rel. 40, Last sequence upd	SULT 1
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SKLEDIERELKDKQAEIKSNQE 1631
                                                                   ELKIQLEKITNLSKAKEKSESELSRLKKTSSEERKNAEEQLEKLKNEIQ-IKNQAFE---
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                         KFAAQLEREFVDGERSLAESQE
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                                                    DLISRINESEKDIEELKSKLRIEAKSGSELETVKQELNNAQEK---IRINAEENTV--LK
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COILED COIL (POTENTIAL).
CHARGED (HYPER-HYDROPHILIC).
DISPENSABLE FOR THE PROTEIN FUNCTION.
ASP/GLU-RICH (ACIDIC).
G -> E (IN REF. 2).
E -> K (IN REF. 2).
V -> I (IN REF. 2).
I -> V (IN REF. 2).
N -> S (IN REF. 2).
N -> S (IN REF. 2).
I -> V (IN REF. 2).
O -> S (IN REF. 2).
I -> V (IN REF. 2).
O -> S (IN REF. 2).
O -> S (IN REF. 2).
O -> CIN REF. 2).
O -> DEEDDEE (IN REF. 2).
C -> S (IN REF. 2).
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Pred.
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No. 0.0
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nes 268;
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RESULT 2
REST_CHICK
                                                                                              Query Match
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EMBL; AF020764; AAC60345.1; -.
EMBL; AF045550; AAC03547.1; -.
EMBL; AF045651; AAC03548.1; -.
InterPro; IPR000938; CAP-G1y.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF01302; CAP_G1y; 2.
SMART; SM0343; Znf_CCHC; 1.
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianidae; Phasia
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                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=98137792; PubMed=9469933;

Gripparic L., Volosky J.M., Keller T.C. III;

"Cloning and expression of chicken CLIP-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restricted the companion of the companion of the contract of the companion o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 206:195-208(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00845; CAP_GLY_1; PROSITE; PS50245; CAP_GLY_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griparic L., Keller
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
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SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS
                                                                                                                          803
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440
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6.5%;
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                                                                                       RKRQISEDPEN (IN ISOFORM 3).
S -> GGSSKVS (IN ISOFORM 3)
T -> RKRQISEDPENT (IN ISOFORM 5)
K -> R (IN REF. 2; AAC03547
E -> V (IN REF. 2; AAC03548
5 MW; 5631CE8683498E23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAP-GLY 1.
                                                                                                                                                                                                                                                                                                                                                                                                 SER-RICH.
CAP-GLY 2.
SER-RICH.
   Score 209;
Pred. No. 0.
                                                                                                                                                                                                                                                                             MISSING (IN ISOFORM 2). TQTKLEHARIKELEQSLLFEKTKADKLQRELEDTR
                                                                                                                                                                                                                                                                                                                                         CCHC-BOX.
                                                                                                                                                                                                                                                                                                                                                                     COILED COIL (POTENTIAL)
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                                                                                                                          -> RKRQISEDPENT (IN ISOFORM
-> R (IN REF. 2; AAC03547).
-> V (IN REF. 2; AAC03548).
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There are no restrictions
ong as its content is in
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                               DB 1;
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Best Local Matches 15

Similarity

Conservative

126;

Mismatches

Indels

342;

Gaps

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RESULT
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                                                                                                   MSB2_YEAST STANDARD; PKI; AUGUSTA PB3334; PB334; PB334; PB334; PB334; PB344; PB344;
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   MSB2 protein (Multicopy suppression MSB2 OR YGR014W. Saccharomyces cerevisiae (Baker's Eukaryota; Fungi; Ascomycota; Sacc
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Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
"Sequence analysis of 203 kilobases from Saccharomyces
Chromosome VII.";
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Bender A., Pringle J.R.;
"A Ser/Thr-rich multicopy suppres
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                                                                                                                                                                                               SNFDTAKSGLENAKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQK 168
                                                                                                                                                                                                                                                     VSSWSFLSSAKNALISL----RDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAK 108
                                                                                                                                                                                                                                                                               NGTQQAQSQSES-----QGQVSFTNEASQDSSTTSLVTAYSQGVHSHQSATIVSATISSL
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                                                           IDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASA
                                                                                   ISASLTTTDSSESFDQTSTAG---AIPVQSSADFSSSSEILVQSSADFSSPSSPTTTDIS
                                                                                                        ISYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKEL
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                                                                -!- SUBUNIT: MUSCLE MYOSIN IS À HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
-!- CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
-!- CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
-!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83273600; PubMed=6576334;
Karn J., Brenner S., Barnett L.;
"Protein structural domains in the Caenorhabditis elegans unc-54
myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonsense mutations via altered Cell 33:575-583(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1876-1966 FROM N.A. MEDLINE=83232892; PubMed=6571695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McLachlan A.D., Karn J.;
"Periodic charge distributions in the myosin match cross-bridge spacings in muscle.";
Nature 299:226-231(1982).
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21-JUL-1986 (Rel. 01, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain B (MHC B).
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SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENT (S2).
MISCELLANEOUS: THERE ARE FOUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin; Muscle protein; Coiled coil; Thick filament; AcATP-binding; Methylation; Alkylation; Multigene family.

DOWALN 1 850 MYOSIN HEAD-LIKE.

DOMAIN 851 1966 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
                                                                                                                                               1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions
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MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT. SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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            --ATAKELQAMEAQLTAMSDQLVGADGELPAE-IQAIKDA--LAQALKQPSADGLATAMG
                                      RAKSDLQR-----ELEELGEKLDEQGGATAAQVEVNKKREAELAKLRRDLEEANMNHENQ
                                                                SAAGALKSSNNSGRISLLLDDVDNEMAATALQ-----
                                                                                          NLKKKESELHSVSSRLEDEQALVSKLQRQIKDGQSRISELEEE-----LENERQSRSKAD
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                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=95345066; PubMed=7619795;
Fisher A.J., Smith C.A., Thoden J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87092266; PubMed-3540939; Warrick H.M., de Lozanne A., Leinwand I Conserved protein domains in a myosin
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  X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE-96206189; PubMed-8611530;
                                                                   Biochemistry 34:8973-8981(1995).
                                                                                                             "X-ray structure of the magnesis
truncated head of Dictyostelium
                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE=95345067; PubMed=7619796;
Smith C.A., Rayment I.;
                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium myosin heavy chain."; FEBS Lett. 227:71-75(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagle G., Noegel A., Scheel J., Gerisch
"Phosphorylation of threonine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerisch G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90353583; PubMed=2387408;
Lueck-Vielmeter D., Schleicher M.,
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01-OCT-1989 (Rel. 12,
16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphorylatable heavy chain fragment FEBS Lett. 269:239-243(1990).
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NCBI_TaxID=44689;
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                                                                                                             the magnesium(II)-pyrophosphate (
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Pfam; PF00063; myosin_head; 1 Pfam; PF00612; IQ; 2. Pfam; PF02736; Myosin_N; 1. PRINTS; PR00193; MYOSINHEAVY PTODOm; PD000355; myosin_head

InterPro; InterPro;

IPR004009; Myosin_N.
IPR001609; myosin_head.

PDB; 1LVK; 28-JAN-98.
DictyDb; DD01008; mhcA.
InterPro; IPR000048; IQ_region.

IVOM;

23-DEC-96.

SMART; SM00015; IQ; 1. SMART; SM00242; MYSC;

myosin_head;

PDB; PDB; PDB; PDB; PDB; PDB; PDB;

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PIR;
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J. Mol. Biol. 274:394-407(197).

-i- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO

ACTIVITY THAT IS ACTIVATED BY ACTIV.
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                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN BE FUR'
SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED

SUBFRAGMENT (S2).

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOW

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEP

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

-!- PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND R

THE ACTIN-ACTIVATED ATPASE ACTIVITY.

-!- MISCELLANEOUS: DICTYOSTELJUM MYOSIN II HAS NO K(2)EDTA ATPAS

ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT TH

POSITION (688).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum myosin motor Biochemistry 35:5404-5417(1996).
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"X-ray structure of the magnesium(II).
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sen the Swiss Institute of Bioinformatics
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33
RESULT 6

NYSA_CAEEL

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ID MYSA_CAEEL

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                                                                    PROSITE;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head
SMARR; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dibb N.J., Maruyama I.N., Krause M., "Sequence analysis of the complete C
                                                   PROSITE; PS50096; IQ; l.
Myosin; Muscle protein; Coiled coil; Thick filament;
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000048; IQ_region.
InterPro; IPR004009; Myosin_tall.
InterPro; IPR002928; Myosin_tall.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X08067; CAA30856.1;
PIR; S02771; S02771.
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Rhabditidae; Peloder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
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                     ATP-binding; Methylation; Alkylation; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain gene family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SUBCELLULAR LOCATION: TRICK FILAMENTS (MLC-2).

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAN SYMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN RE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS:
C.ELEGANS.
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                                                                                                                                                                                                                                                       PF00063; myosin_head; 1.
PF00612; IQ; 1.
PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                            PF02736; Myosin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P08799;
                                                                                 PS50096; IQ;
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9 (Rel. 12, Last sequ
1 (Rel. 40, Last anno
vy chain A (MHC A).
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                                                                                                                                                                      myosin_head;
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annotation
MYOSIN HEAD-LIKE
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Caenorhabditis
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RESULT 7
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Best Local S
Matches 142
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Q04893;
Q1-NOV-1997
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                                                                                                                                                                                                           GERSLAESQENAFRKQPAFIQQVLVNIASLFS
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(Rel. 35, Last annotation update)
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METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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-!- DOMAIN: CONTAINS MANY SER/THR-RICH DOMAIN AND REPEATS
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Repeat. SEQUENCE 1140 AA; 113070 MW; 0153EBCA24FE5427
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Matches 136
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SMART; SM00027; EH; 3.
SMART; SM00165; UBA; 1.
PROSITE; PS50031; EH; 3.
Hypothetical protein; Repeat.
DOMAIN
14 113 EI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy "Sequencing and functional analysis of a 32,560 bp segment on the left arm of yeast chromosome II. Identification of 26 open reading frames, including the KIP1 and SEC17 genes.";
Yeast 9:1355-1371(1993).
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01-OCT 1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 150.8 kDa protein in SEC17-QCR1
YBL047C OR YBL0520 OR YBL0501.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S0000143; YBL047C.
rPro; IPR000261; EPS15_repeat.
rPro; IPR000449; UBA_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 235808; CAA84867.1; -.
; X78214; CAA55048.1; -.
; Z23261; CAA80797.1; -.
$45781; S45781.
HSSSGLKKFTPTSNFGQSIIKEEPEEQEQLRESSDTFSAQPPPVPKHASSPVK---
                                              HMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASP----SASSSVSSWSFLSS
                                                                                                                                                                                                                                                                                                                                                                                                                           PF00036; efhand; 2. PF00627; UBA; 1.
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Jacques B., Jon
                                                                                                                                                                                                                             113
227
366
                                                                                                                                                                                                13 EH
227 EH
66 EH
150783 MW;
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                                                                                                                          Score 199.5;
Pred. No. 0.
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H 2.
H 3.
; 626FD261DCBA7D99 C
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                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
15-JUN-2002 (Rel. 41,
Hypothetical protein (
SPACIF3.06C.
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart Sgourcs J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G Holroyd S., Hornsby T., Howarth S., Huckle E.J., Huth S., Jagels James K., Jones M., Leather S., McDenald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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NCBI_TaxID=4896;
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                                                                                                                                                            MEDLINE=21848401; PubMed=11859360;
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RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Vanstreels E., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Golibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Charles Sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 --- ANYSDAIVHK--- DKLIEDLSTR-ISEFDNLKSERDTLSIKNE--- KLEKLLRNTIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 NPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRDAILNKNSSPTD
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NNHQTITKQLKDTSSKLQQLQLERANFEQKESTLSDENNDLRTKLLKLEESNKSLIKKQE
                                                                              SGVQSAISQ---TANPALSRSVSRSG------
                                                                                                                                                         EAAVATNNELSESKNSLQTLCNAFQEKLAKSVMQLKENEQNFSSLDTSFKKLNESHQELE
                                                                                                                                                                                                                                                                                                                   RDILNEKKKHEVYESQLNELKGELQTEIS------NSEHLSSQLS--TLAAEK
                                                                                                                                                                                                                                                                                                                                                                                      AQL-----TAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAK
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Pred. No. 0.44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle myosin heavy chain gene from Acanthamoeba: evidence of a hinge in the rodlike tail.";
J. Cell Biol. 105:913-925(1987).
-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
-I- SUBUNIT: MYOSIN II HEAVY CHAIN IS TMO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
PROSITE; PS50096; IQ: 1.

Myosin; Colled coil; Actin-binding; ATP-binding; Cal
Methylation; Alkylation; Phosphorylation; Multigene
DOMAIN 1 789 MYOSIN HEAD-LIKE.
                                                                                                                              SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
                                                                                                                                                                                       Pfam; PF00612; IQ; 2.
Pfam; PF02736; Myosin_N; 1.
PFINTS; PR00193; MYOSINHEAVY.
PF000m; PD000355; Myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y00624; CAA68663.1;
PIR; A27224; A27224.
HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                              InterPro;
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COMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HETTAPETIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILPIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.

MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 2 IQ DOMAINS.
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                                                                                                                                                                                                                                                                                                                                PF00063;
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IPR004009; Myosin_N.
IPR001609; myosin_head
0063; myosin_head; 1.
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                                             RRLLAEIEELKKRVAKETSDKQKAQDQKA-----NYQRENESLKADRDSIERRNRDAER
                                                                  --LMSTIVSNPQANQEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGER
                                                                                          EKNLDKANLELEELRQEADDAARDNDKLVKDNRKLKADLDEARIQLEEEQDAKSHADSSS
                                                                                                               SRSVSRSGIESQ--GRSADASQRAAETIVRDSQTL-GDV-YSRLQV------LDS--
                                                                                                                                      RDSGAQQRRKLNTRISELQSELENAPKTGGASSEEVKRLEGELERLEEELLTAQEARAAA
                                                                                                                                                          LSDGYSAYKTLNSLYSESRSGVQSA--
                                                                                                                                                                                                        ALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTS--SSSYAAA
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                                                                                                                                                                                                                                                                            LEEEK-SGKE----AASSKAKQLGQQLEDARSEVDSLKSKLSAAEKSLKTAKDQN-----
                                                                                                                                                                                                                                                                                                 IQEIKPSGSDIPIVGPSGSAASAG-----SAAGALKSSNNSGRISLLLDDVDNEMAAI
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                                                                                                                                                                                                                                                                                                                                             TKE-LIDA---AETKVNELKQEHTGLTD-----SPLVKKAEEQISQAQKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 199; DB Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION (TRI-) (POTENTIAL) ALKYLATION (SH-1) (POTENTIAL). PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGHT MEROMYOSIN (LMM).
ALPHA-HELICAL TAILPIECE.
NONHELICAL TAILPIECE.
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COILED
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J. Mol. Biol.
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P12847;
01-OCT-1989
01-OCT-1989
DOMAIN
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                                                                                                                                          PRINTS; PR00193; MYOSINHEAVY.
PTODOM; PD000355; myosin_head;
SMART; SM00015; TQ; 1.
SMART; SM000442; MYSC; 1.
PROSITE; PS50096; TQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X04267; CAA27817.1; -. PIR; A24922; A24922. HSSP; P13538; 2MXS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=87060988; PubMed=3783701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin heavy chain, fast skeletal muscle, embryonic
                                                                                                                                                                                    Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                                                                                   Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                          DOMAIN
                                                                                                                                   Multigene family.
                                                                                                                                                            Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                             PF00063; myosin_head; 1.
PF00612; IQ; 2.
PF01576; Myosin_tail; 1.
PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002928; Myosin_tail.
IPR002017; Spectrin.
IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR004009;
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Myosin_N.

Myosin_tail.
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IQ.
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                          MYOSIN
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                                                                                                          HEAD-LIKE
                                                                                                                                                                                       Thick filament; Actin-binding;
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01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
ALKYLATION (SH-2).
MW; B5D546A596E5A696 CRC64;
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Pfam; PF01608; I_LWEQ; 1.
ProDom; PD011820; IWEQ; 1.
SMART; SM00295; B41; 1.
SMART; SM00295; B41; 1.
SMART; SM00307; ILWEQ; 1.
PROSITE: PS00660; BAND_41_1; 1
PROSITE: PS00661; BAND_41_2; 1
PROSITE: PS50057; BAND_41_3; 1
 2175
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DOMAIN 134 294 BAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kreitmeier M., Gerisch G., Heizer C., Mueller-Taubenberger A.; "A talin homologue of Dictyostelium rapidly assembles at the leading edge of cells in response to chemoattractant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                     TAEIFAQSARDLAKSSI-EIVTSYTSSQDS-LVKSSQAVVSNVQSFISNSK
                                                                                                            SLGKSAEAVAEA - - - VGQFLTSVYTAISDAGKGIKELEKSIVQVANYHEKPDTVLSNKDA
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-GVIALLGNGNDDLKSKVLENVKQTTGDMLALLQCVKDQDKNGSTSIADATRSISDRV 2231
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01-FEB-1995 (Rel. 31, Last sequence update
16-OCT-2001 (Rel. 40, Last annotation upda
Myosin heavy chain, clone 203 (Fragment).
                                                                                                                                                                                                                                                                          DOMAIN
NON_TER
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Pfam; PF01576; Myosin_tail; 1.
Myosin; Muscle protein; Coiled co
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Submitted (SEP-1994) to the
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NCBI_TaxID=6087;
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DSLSQLEASTSTVTRVAAKDYDEAKSNEDTAKSGLENAKTLAEYETKMADLMAALQDM
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01-MAR-1992 (Rel. 21, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Myosin heavy chain, striated muscle.
Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia;
                                                                                                                                                                                                                                                                                                                                                                                                                                chain. Sequence comparison with other heavy that might be critical for regulation."; J. Biol. Chem. 266:18469-18476(1991).
                                                                             Xie X., Harrison D.H., Schlichting I.,
Szent-Gyorgyi A.G., Cohen C.;
                                                                                                                                                                                                                                                                   Nyitray L., Goodwin E.B., Szent-Gyorgyi "Nucleotide sequence of full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Adductor muscle;
MEDLINE=92011595; PubMed=1917970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pectinoidea; Pectinidae; Argopecten NCBI_TaxID=31199;
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                                                                                                                                 MEDLINE=94173332; PubMed=8127365;
                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
                                                                                                                                                                                                                 Nucleic Acids Res.
                                                                                                                                                                                                                                          muscle myosin
                                                                                                                                                                                                                                                                                                                       MEDLINE=91088319; PubMed=2263488;
                                                                                                                                                                                                                                                                                                                                                     TISSUE-Adductor muscle;
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"Structure of the regulatory

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Best Local Similarity
Matches 148; Conser
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Pfam: PF00175; NYOsin_tail; 1.
Pfam: PF01576; Myosin_tail; 1.
Pfam: PF02736; Myosin_N: 1.
Pfam: PF000193; MYOSINHEAVY.
PRINTS; PR001935; myosin_head; 1.
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SMART; SM000242; MYSG; 1.
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                                                                                                                                                                                                                                                                                                                                                          Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Alkylation; Calmodulin-binding; 3D-structure.

DOMAIN 1 777 MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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InterPro; IPR004009; Myosin_t.
InterPro; IPR002017; Spectrin.
InterPro; IPR001609; Myosin_head.
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X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 777-836.
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SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SUBLELIARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 10 DOMAIN.
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1WDC; 11-JUL-96.
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                                                                                                               KDYDEAKSNFDTAKSGLENAKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIK
                                        LSEAEQTTEAANAKCSALEKAKSRL------QGELEDMS-IEVDRANASVNQMEK 1441
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COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
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                                              RAKSRSSVSVQRSSVSVSA 1936
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RC MEDLINE-93028466; PubMed=1409643;
Garcia J.A., Ou S.-H.I., Wu F., Lusis A.J., Sparkes R.S., Gaynor R.B.
"Cloning and chromosomal mapping of a human immunodeficiency virus 1
'TATA' element modulatory factor.";
Proc. Natl. Acad. Sci. U.S.A. 89:9372-9376(1992).
-!- FUNCTION: THIS PROTEIN BINDS THE HIV-1 TATA ELEMENT AND INHIBITS
TRANSCRIPTIONAL ACTIVATION BY THE TATA-BINDING PROTEIN (TBP). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; TMF1_HUMAN TISSUE-Cervical carcinoma; SEQUENCE FROM N.A., AND FUNCTION. Homo sapiens (Human) TATA element 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update) NCBI_TaxID=9606; P82094; modulatory STANDARD; factor (TMF). PRT; Catarrhini; Hominidae; Craniata; Vertebrata; Euteleostomi; 1093 AA

between the Swiss Institute of Bloinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us This SWISS-PROT entry is copyright. It is produced through a collaboration requires a license agreement (See http://www.isb-sib.ch/announce/ There are no restrictions on ong as its content is in no oved. Usage by and for comme and the EMBL outstation way its

Gaynor R.B.; ncy virus 1

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16-OCT-2001 (
Myosin heavy
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EMBL;
EMBL;
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karsch-Mizrachi I., Travis M., Blau H., Leinwand "Expression and DNA sequence analysis of a human muscle myosin heavy chain gene.", Nucleic Acids Res. 17:6167-6179(1989).
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MEDLINE-89263803; PubMed=2726495;

Eller M.S., Stedman H.H., Sylvester J.E.,

Rubinstein N.A., Kelly A.M., Sarkar S.;

"Nucleotide sequence of full length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 774-1940 FROM N.A. MEDLINE-90033298; PubMed-2806546; Eller M.S., Stedman H.H., Sylvest
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                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 856-1940 FROM N.A. MEDLINE=89366648; PubMed=2771643;
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Bober E., Buchberger-Seidl A., Braun
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Mammalia;
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                                                                                                                                                                                                                                                                                                    DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDE: CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MENOMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                             SUBFRAGMENT (S2).
SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSIST HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELETAL AND NOT PRESENT OR BARELY DETECTABLE IN HEART AND ADULT SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biochem.
X13988;
X13100;
X51593;
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(Rel. 40, Last annotation updat
y chain, fast skeletal muscle, e
y chain) (SMHCE).
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hem. 189:55-65(1990).
CAA32167.1;
CAA31492.1;
CAA35942.1;
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InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_head.
InterPro; IPR001609; Myosin_head.
InterPro; IPR001609; Myosin_head.
Pfam; PP000612; IQ; 2.
Pfam; PP001576; Myosin_head; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF02736; Myosin_N; 1.
PRAWTS; PR00193; MYOSINHEAVY.
PRODOM; PD000155; MYOSINHEAVY.
PRODOM; PD00015; IQ; 1.
SMART; SM000142; MYSS; 1.
SMART; SM000142; MYSS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calmodulin-binding; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50096; IQ; 1. Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
  425
                                                                                                                                        263
                                                                                                                                                                                                                                                                               105
                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                      8 MESGPESVSSNQSSMNPI---INGQIA----SNSETKES------TKASEASPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x15696;
S04090; S
: P13538;
                                                                                       QRDTQEIKPS-----GSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEM
                                                                                                                                                                          QIIKDLERQNI------SYEAVLT---NAGEVIKASSEAGIKLGQALQSIVDAGDQ :: |:|| | | | | | | | | | | |
                                                                                                                                                                                                                        ALEAQKDTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQ---LEINK----NSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160720; -.
  AIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSAG---
                      DRKIAEKD--EEIEQLKRNYQRTVETMQSALDAEVRSRNEAIRLKKKMEGDLNEIEIQLS
                                    -AAIALQGFRSMIEQFNVNNPATAKELQ-AMEAQLTAMSD-----
                                                                    GKTIHELEKSRKQIELEKADIQLALEEAEAALEHEEAKIL---
                                                                                                                                       SQAAVLQAQQNNSPDNIAATKELIDAAETKVNE----LKQEHTGLTDSPLVKKAEEQISQA
                                                                                                                                                              DLMVDVERANSLAAALDKKQRNFDKVLAEWKTKCEESQAELEASLKESRSL--
                                                                                                                                                                                                           QEGKAELQRALSKANSEVAQWRTKYETD-----AIQ-----RTEELEEAKK
                                                                                                                                                                                                                                                                                                   LEEKESIVSQLSRSKQAFTQQTEELKRQLEEENKAKNALAHALQSSRHDCDLLREQYEEE
                                                                                                                                                                                                                                                                                                                         ASSSVSSWSFLSSAKNALI----SLRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDY 104
                                                                                                                                                                                                                                                                                                                                               LSSSMESVSKSKANLEKICRTLEDQLSEARGKNEEIQRSLSELTTQKSRLQTEAGELSRQ
                                                                                                                --STELFKLKN-----AYEEALDQLETVKRENKNLEQEIADLT-----EQIAEN
                                                                                                                                                                                                                                                                           DEAKSNEDTA - - KSGLENAKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKK 162
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      782
840
179
656
758
130
696
706
1331
1331
1608
                                                                                                                                                                                                                                                                                                                                                                                              Conservative 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S04090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA33731.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2MYS
                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      781
811
1933
186
678
678
772
130
696
1331
1332
1609
                                                                                                                                                                                                                                                                                                                                                                                                       6.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                           224035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                          KK -> QE (IN REF. 1
SR -> RA (IN REF. 3
RG -> QT (IN REF. 2
5 MW; 43CA58C6A4BA125
                                                                                                                                                                                                                                                                                                                                                                                                        Score 194; DB Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALKYLATION (SH-1)
ALKYLATION (SH-2)
A -> G (IN REF. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHYLATION (TRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          43CA58C6A4BA1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                              265;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Indels 194;
                                             -QLVGADGELPAEIQ
                                                                    RIQLELTQVKSEI
  TAGTVQMNV
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                     1573
                                                                                                                                       319
                                                                                                                                                                                                           1427
                                                                                                                                                                                                                                                       1392
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                                                                                                                                                                                                                                                                                                                                                 1291
                        1631
                                              424
                                                                                                                  1520
                                                                                                                                                              1478
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RELEMBO J. 10:2479-2488(LIJIA).

CC -I- FUNCTION: MUSCLE CONTRACTION.

CC -I- SUBUNIT: MUSCLE MYSSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC -I- SUBUNIT: MUSCLE MYSSIN IS A HEXAMERIC PROTEIN THAT CONSISTS (MLC)

CC -I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils and consistent of the myofibrils.

CC -I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils and consistent of the myofibrils.

CC -I- ALTERNATIVE PRODUCTS: At least 15 isoforms; AAAAA (shown here),

CC BDBBA, BABDB, 3b, 7b, 7c, 7d, 9b, 9c, 11b, 11c, 11d, 11e, 15b and

CC BDBBA, BABDB, 3b, 7b, 7c, 7d, 9b, 9c, 11b, 11c, 11d, 11e, 15b and

CC BDBBA, BABDB, 3b, 7b, 7c, 7d, 9b, 9c, 11b, 11c, 11d, 11e, 15b and

CC BDBBA, BABDB, 3b, 7b, 7c, 7d, 9b, 9c, 11b, 11c, 11d, 11e, 15b and

CC BDBBA, BABDB, 3b, 7b, 7c, 7d, 9b, 9c, 11b, 11c, 11d, 11e, 15b and

CC BDBBA, BABDB, 3b, 7b, 7c, 7d, 9b, 9c, 11b, 11c, 11d, 11e, 15b and

CC TAITERNATIVE PRODUCTS At least 15 isoforms; AAAAA (shown here),

CC TAITERNATIVE PRODUCTS At least 15 isoforms; AAAAA (shown here),

CC TISSUE SPECIFICITY: Expressed in larval and adult muscles.

CC TISSUE SPECIFICITY: Expressed in larval and adult muscles, exons 9b

TO muscles, exons 9a and 9b are expressed in jump muscles, exons 9b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 17
                                                 Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
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                                                                                                                                                                                                                                                                                                                                  Kronert W.A., Edwards K.A., Roche E.S., Wells L., E "Muscle-specific accumulation of Drosophila myosin splicing mutation in an alternative exon results in substitution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87280141; PubMed=3038896; MEDLINE-87280141; PubMed=3038896; MEDLINE-87280141; MEDLINE-87280141; MEDLINE-87280141; MEDLINE-87280141 MEDLINE-8728014 Neavy chain "Analysis of the 5' end of the Drosophila muscle myosin heavy chain gene. Alternatively spliced transcripts initiate at a single site are funtron locations are conserved compared to myosin genes of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                George E.L., Ober M.B., Emerson C.P. Jr.; "Functional domains of the Drosophila melanoga heavy-chain gene are encoded by alternatively Mol. Cell. Biol. 9:2957-2974(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE STRAIN=Canton-S; TISSUE=Pupae; MEDLINE=89384556; PubMed=2506434;
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Canton-S; TISSUE=Embryonic MEDLINE=91330870; PubMed=1907912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-264 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandbulata; Pancrustacea;
Insecta; Pteryyota; Neoptera; Endopterygota; Diptera; Brach
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 333-614 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYSA_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1988 (Rel. 09, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P05661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQTVKDLQHRLDEAEQL---ALKGGKKQIQKLETRIRELEFELEGEQKKNTESVKGLRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQL-EREF-VDGERSLAESQENAFRKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETDLMQLQSEVEDASRDARNAEEKAKKAITDAAMMAEELKKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQLYKTAFSSTSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem. 262:10741-10747(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RATLEQTERARKLAEQELLDSNERVQ--LLHTQNTSLIHTKKKL 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LRSVQGQLKDTQLHLDDALRGQEDLKEQLAIVERRANLLQAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jr.;
a melanogaster muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spliced exons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- DT-
                                                                                                                                                                                                                                                                                                                                                              in heavy chains: in an isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin
                                                                                                                               , y, 11 and
included
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                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1844
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Pfam; PFUVVVI

R Pfam; PF0061; IQ; 2.

R Pfam; PF01576; Myosin_tail; 1.

PR Pfam; PF02736; Myosin_N; 1.

DR PRINTS; PR00193; MYOSINHEAVY.

DR ProDom; PD000355; myosin_head; 4.

DR SMART; SM00015; IQ; 1.

PP0SITE; PS50096; IQ; 1.

PP0SITE; PS50096; IQ; 1.
               VARSPLIC
                                                                                                                                                                                                                                                                                                      DOMAIN
NP_BIND
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0002741; Mhc.
InterPro; IPR000048; IQ_region.
InterPro; IPR004009; Myosin_N.
InterPro; IPR001609; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                             VARSPLIC
                                                                                                                                          VARSPLIC
                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                   Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Calmodulin-binding; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3L; M61229; AAA28686.1; -.

3L; M61229; AAA28687.1; -.

3L; J02788; AAA28706.1; -.

3L; J02788; AAA28707.1; -.

3L; X60196; CAA42752.1; -.

3L; X60196; CAA42753.1; -.

3L; X60196; CAA42754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and 9c are expressed in other larval and adult muscles.

DOMAIN: Alternative splicing exons contribute to the specialized contractile activities of different muscle types. Exon 3 encodes the hydrophobic pocket adjacent to the ATP-binding site, exon 9 is adjacent to the actin-binding domain, exon 11 is involved in actin-binding, exon 15 in the S2 hinge and exons 18 and 19 the non-coiled tail region.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P08799; 1MND
                                                                                                                                                                                                                                                                                                                                                                                      family.
             469
                                                                                                                                                                                                                                                                                                         780
802
179
69
                                                                                             469
                                                                                                                                          298
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                                                                                                                                                                                                                                           298
                                                                                                                                                                                                                                                                                                         779
809
1927
186
116
                                                                                             525
                                                                                                                                                                                                                                           332
                                                                          CFLSDNIYDYYNVSQGKVTVPNMDDGEEFQLAD (IN ISOFORM 7D AND ISOFORM BDBBA).
YNGFEQLCINFTNEKLØGFFNHIMFVMEQEEVKKEGINWDF IDFGMDLLACIDLIEK -> YNGFEQLCINFTNEKLQQFFN
                                                                                                                                       DICLLTDNIYDYHIVSQGKVTVASIDDAEEFSLTD ->
VFLGQHIGDYPGICQGKTRIPGVNDGEEFELTD (IN
ISOFORM 7C).
DICLLTDNIYDYHIVSQGKVTVASIDDAEEFSLTD ->
                                                                                                                                                                                                                     ISOFORM BDBBA AND ISOFORM BABDB).
DICLLTDNIYDYHIVSQGKVTVASIDDAEEFSLTD
CLLSNNIYDYRIVSQGKTTIPSVNDGEEWVAVD (I
                                                                                                                                                                                                                                                                                                                     MYOSIN HEAD-LIKE.
IQ.
COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                       VRDIKSEKVEKVNPPKFEKIEDMADMTVLNTPCVLHNLRQR
YYAKLIY -> TRDLKKDLLQQVNPPKYEKAEDMSNLTYLN
                           BABDB)
                                                         IDFGMDLLACIDLIEK -> YNGFEQLCINFTNEKLQQFFN
HHMFVLEQEEYKREGIDWAFIDFGMDLLACIDLIEK (IN
                                                                                                                                                                                                                                                                      DASVLHNLRQRYYNKLIY (IN ISOFORM 3B,
          YNGFEQLCINFTNEKLQQFFNHIMFVMEQEEYKKEGINWDF
                                            ISOFORM
                                                                                                                                                                                                         ISOFORM 7B)
                                            9B,
                                            ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as its content
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                                            BDBBA
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                                            AND
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                                            ISOFORM
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Qу	Qy	Оy	Оу	Оу	Qy Db	Ф	Qу	Оу	Ду	Qy Db	M B Q	SO 5 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		7 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 H H H H	7 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
575 1347	515 1293	455 1246	399 1192	346 1143	298 1088	238 1049	180 997	128 938	82 888	22 835	Query Match Best Local Matches 14	VARSPLIC VARSPLIC CONFLICT CONFLICT CONFLICT SEQUENCE	VARSPLIC	VARSPLIC	VARSPLIC	VARSPLIC
EEEAEG	AISQTANP : AESQVSQL	KVGGGS : KIAKQL	QAME : RKKHND	EELGER	QEHTGL SITAKL	VIKASS KSKRKV	LQNQNKSLT- : : MQGETNQKTG	ETKMAD- : QKKKADQ	DSLSQL DSLSG-	MNPIIN : :: VKPLLN	sir 2;			TIC	LIC	TIC
KADLQRQL	NPALSRSV ; ; QLSKIKIS	AGTAGT QHTLNE	QAMEAQLTAMSDQL : :: RKKHNDAVAEMAEQVDQL	GSAAGAL EELGERLEEAGGA-	LTDSP-L : LEDEQVV	KASSEAGIKL : KRKVEGDLKL	SLTE QKTGEE	四 1	EASTST	GQIASN ; VSRIED	nilarity Conserva	1936 1937 43 68 215 1962 AA	1216	N I	723	723
S i	SVSRSG: : ISLTTQI	KVGGGSAGTAGTVQMNVKQLYKTAF : ; ; ; KIAKQLQHTLNEVQSKLDETNRT	AMSDQLI EQVDQL	KSSN	VKKAEE(: VLKHQR(GQALQS	VLKTTD: : ! LQAAED!	LMAALQDME :: : LKKDIEDLE	STVTRVI : EKGI	SETKES! : EIARLE!	Ε.Σ	1936 1962 44 68 215	1241	761	761	761
VSNPQA : : KANAEAQVWRS	SRSGIESQGRSAD : : LTTQLEDTKRLAD	OLYKTAI : ; ; ETNRT	VGADGEI : NKI	NSGRISL : TSAQIEL	DISQAQE : DIKELQE	IVDAGDO	SADQIP <i>I</i> : : KINHLNF	ME RI : : LELNVQF	AAKDYDI : ALQDYQI	TKASEAS : EKAKKAI	1%; 1%; 10	P MI EK E E L L L 24480 MW;	+ F > X		· · · · · ·	
RSKYESDG	ASQ EES	SSTSSS	AQLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSAD ::	מעפטזי	EHTGLTDSP-LVKKAEEQISQAQKDIQEIKPSGSDIP 	VIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAET 	-EVLKTTDSADQIPAINSQLE - : : :: EELQAAEDKINHLNKVKAKLE	LMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVT 	DSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAKSGLENAKTLAEY 	MNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRDAIL 	Score 194; DF Pred. No. 0.74 6; Mismatches	- V - SS - V	K (IN ISOFORM 11E). AEHDROTCHNELNQTRTACDQLGRDK LINDLRAGVDHITNEK (IN ISOFORM	-> TKIMCPKLLQGVEKDKKATEIIIKEIDLPEDQYRLGNT K (IN ISOFORM 11D AND ISOFORM BARDB) YQILNPRGIKDLDCPKKASKYLIESTELNEDLYRLGHTK -> YMILABAIMAAEKVAKNAAGKCLEAVGLDPDMYRIGHT	((IN I	IDFGMDLLACIDLIEK -> YNGFEQLCINFTNEKLQQFFN HHMFVLEQEEYQREGIEWTFIDFGMDLQLCIDLIEK (IN ISOFORM 9C). YQILNPRGIKDLDCPKKASKVLIESTELNEDLYRLGHTK -> YQILNPAGIVGVDDPKKCGSIILESTALDPDMYRIGHT
VARSE	RAAETIVI	SYAAALSDGYSAYKTLNSLYSES : :: : LNDFDASKKKLSIENSDL	IKDALA ; DRQTCH	NEMAAIALQGFRSMIEQFNVNNPATAKEL 	PSGSDI	QAQQNN: :: DLERNK	INK	NNHTEE : TK-DHQ:	TAKSGLE : AQKNDLE	VSSWSFI VKVRKEI	194; DB No. 0.74; smatches	(INI) (INI) (INI) (INI)	ISOFORM 11E) TCHNELNOTRTA GVDHITNEK (I	CPKLLQ CPKLLQ SOFORM GIKDLD APAIMA	SOFORM GIKDLD GIKDLD NPKGIK SOFORM	LACIDL: QEEYQR! 9C). GIKDLDO
NQEEIMO	RDSQTLO	LSDGYSAYKTLNSLYSESRSGVQ : :: : :DPFDASKKKLSIENSDLLRQLE	QALKQPS NELNQTF	ALQGFRS ELSKLRF	PIVGPSGSAAS : ; ; -VEAERQARAK	SPDNIAA	NSADQIIKDLE: -	TEEVNNIKKALEAQKDTIDKLNKLVT :: : : : DHQIRNLNDEIAHQDELINKLNKEKK	EN	LSSAKN <i>I</i> : LEALNAF	1; 282;	N ISOFORM 1 I ISOFORM 1 I ISOFORM 2) IN REF. 2) REF. 2). REF. 2).	11E). OTRTACI EK (IN	GVEKDKE 11D AN CPKKASE	11B AN CPKKASH GIEDPKH 11C).	IEK -> EGIEWTE
EIMQKLTASISK 	GDVYSRLQVLDSLMSTI : : KFRNLEHDLDNLREQV	KTLNSL : KKLSIE	ADG	MIEQFN : : DLEEAN	IVGPSGSAASA : ; VEAERQARAKAEKQRADLARE	TKELID	ERQNIS	LEAQKD: : : CIAHQDE	QERLTQ	LISLRD :::: (LLAEKT	Length 1 Indels	.8). 18).)QLGRDK ISOFOR	(ATEIII ID ISOF	ID ISOF	YNGFEQ
APQF : AEE-	QVLDSL : HDLDNL	YSESRS : NSDLLR	ADGLATAMGQVAFAAA ; ; TACDQLGRDKAAQE	VNNPAT : : : IQHEST	KQRADL	KELIDAAETKV : KELEQTIQRKD	RQNISYEAVLTNAG 	TIDKLN : LINKLN	AKT : EEDARN	L	962; 176	••	-> AE M 15B	KFIDLP ORM BA ELNEDL EAVGLD	ORM BD ELNEDL ESTELN	LCINET LQLCID ELNEDL ESTALD
GYPA 6	< ⊢	S EE		L - L	L 3	TKVNELK 2	H — H	9 1		SPT 8	; Gaps		AEKEKNEYYGQ B AND	EDQYRL BDB). YRLGHT	BBA). YRLGHT DDQYRL	NEKLQQ LIEK (YRLGHT: PDMYRI
405	574 1346	514 1292	454 1245	191	145	087	237 1048	79 96	127 937	1 87	s 26;		YGQ	LGNT LGNT	S GNT	SHT IN EFN

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1406

LNQKCIGLEKTKQRLSTEVEDLQLEVDRANAIANAAE---KKQKAF VQNSADSLQKFAAQLEREF-----VDGERSLAESQENAFRKQPAF

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RESULT 18
WYHD_HUMAN
ID MYHD_H
AC Q9UKX3
DT 16-OCT
DT MYH13.
OS HOMO S
OC ENKARY
OC Mammal
OX MEDLIN
RA Weiss
RT "COmpa
RT HESUEN
RA Winter
RT "The heavy
RL J. MOL
RT Genomi
CC -!- SU
CC -!- FU
CC -!- FU
CC -!- FU
CC -!- FU
CC -!- SU
CC -!- FU
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Q9UKX3; 095252;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Skeletal muscle, extraocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99026150; PubMed-9806854; Winters L.M., Briggs M.M., Schachat F.; "The human extraocular muscle myosin heavy chain the cluster of fast and developmental myosin gene Genomics 54:188-189(1998).
                                                                                                                                                           InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                EMBL; AF111782; AAD29948.1; -. EMBL; AF075248; AAC83241.1; -. HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99318869: PubMed-10388558; Weiss A., Schiaffino S., Leinwand L.A.; Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity."; J. Mol. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Extraocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Extraocular muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYHD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1917-1938 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELLCAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELLCAL COILED COILS.

PYM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT BURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: MUSCLE CONTRACTION
                                                                                             PF00063; myosin_head; 1. PF00612; IQ; 2.
                                                                                                                                                                                                                                                                                                                      HGNC:7571; MYH13.
                                                                                                                                                       IPR000048; IQ_region.
IPR004009; Myosin_N.
IPR002928; Myosin_tail.
IPR001609; myosin_head.
                                Myosin_tail; 1.
Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
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genes on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MYH13) maps to chromosome 17.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration -
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RESULT 19
ALM1_SCHPC
ID ALM1_
AC Q9UTK
DT 16-OC
DT 15-JU
DE Abnor
GN ALM1
OS Schiz

SCHPO

ALM1_SCHPO STANDARD; PRT; 1727 AA Q9UTK5; 013313; Q9UTT8; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Abnormal long morphology protein 1 (Sp8).

update)

AA.

Abnormal long morphology protein 1 ALM1 OR SPAC1486.04C.

Schizosaccharomyces pombe (Fission yeast)

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Best Local
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1322
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MOD_RES
MOD_RES
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                                                                                                         1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00015; 10;
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                                                      1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                             386
                                                                                                                                                                                                                                                                                                                                                                                                             219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AAKDYDEAKSNEDTAKSGLENAKT-LAEYETKMADLMAALQDMERLANSDPSNNHTEEVN 158
                                                   EIKAKDEQQTQLIHDLNMQKARLQTQNGELSHRVEEKESLISQLTKSKQALTQQLEELKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIKKALEAQKOTIDKLNKLYTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQII
QMEEETKAKNAMAHALQSSRHDCDLLREQYEEE - - - - QEAKAELQ
                                                                                                     VAELGEQIDNLQRVKQKLEKEKSELKMEIDDMASNIEALSKSKSNIERTCRTVE--DQFS
                                                                                                                                                                                                                    DEQVHSLQFQKKIKELQARIEELEEE-IEAEHTLRAKIEKQRSDLARELEEIS-----
                                                                                                                                                                                                                                                                       -----ERAKRKLEGDLKMSQES-----IMDLENEKQQIEEKLKKKEFELSQLQARID
                                                                                                                                                                                                                                                                                                                             LDD-----LQVEEDKVNGLIK-----INAKLEQQTDDLEGSLEQEKKLRADL-
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                                                                                                                                                                                                                                                                                                                                                                                   SSLKRDIDDLELTLTKY-EKEKHATENKVKNLSEEMTALEENISKLTKEKKSLQEAHQQT 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LMDAEERCEGLIKSKILLEAKVKELTERLEEEEE-----MNSELVAKKRNLEDKC
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                         LTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQ
                                                                               ETIVRDSQTL:
                                                                                                                                 -AALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQRAA
                                                                                                                                                              -----ERLEEASGATSAQIEMNKKREAEFQKMRRDLEEATLQHEATAATLRKKQADS
                                                                                                                                                                                         MGQVAFAAAKVGGGSAGTAGTVQMNVKQ-----
                                                                                                                                                                                                                                             QFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATA
                                                                                                                                                                                                                                                                                                  IVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAI-----ALQGFRSMIE
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L5; Conservative 111;
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814
1938
186
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709
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COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHYLATION (TRI-) (POTENTIAL)
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                            -GDVYSRLQVLDSLMSTIVSNPQA--NQEEIMQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1F6D006416381CD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Length 1938;
                                                                                                                                                                                          --LYKTAFSSTSSSYA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 122;
1362
                           633
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RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rajor K., Jaylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moesfer M., Hilbert H.,
RA Borrym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moesfer M., Mueller-Auer S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Forsburg S.L.,
RA Goffeau A., Cadieu E., Bento J.,
                                                                                                                       EMBL;
                                                                                                                                                                                                 entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                "Large-scale screening of intracellular protein localization in liveristic protein screening of intracellular protein localization in livery fission years cells by the use of a GFP-fusion genomic DNA library Genes Cells 5:169-190(2000).

-i- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE.

CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20223868; PubMed=10759889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jimenez M., Petit T., Gancedo C., Goday C.;
"The alml+ gene from Schizosaccharomyces pombe
protein that associates with the medial region
Mol. Gen. Genet. 262:921-930(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                      DOMAIN
                                                           DOMAIN
                                                                                DOMAIN
                                                                                                    Coiled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20123449; PubMed=10660053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 495-1727 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21848401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ום.ם.,
                                                                                                                                       AL133357;
AF010473;
                                                                                                                   AB028012;
                                                                                                    COIL.
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  57
443
542
804
1223
                                                                                                                     ; CAB62414.1;
; AAB65416.1;
; BAA87316.1;
  361
463
740
1106
1427
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COIL
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                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                        Usage
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genomic DNA library.
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mitosis.
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Best Local
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DOMAIN
SEQUENCE
                                                                                                                                                                   MYH4_RABIT
Q28641;
                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                            Myosin heavy chain, skeletal muscle, juvenile
              STRAIN-New
                            SEQUENCE FROM N.A.
                                                                                            Oryctolagus cuniculus
                                                                                                                                                                                                                                                      683
                                                                                                                                                                                                                                                                                603
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                                                                                                                                                                                                                                                      ELENS----
                                                                                                                                                                                                                                                                             AVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAFTQQVLVNTASLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHSKVCEKLEVSSRQVQDLEKKLAGLAQQNTELNEKIQLFEQKRSNYSSDGNISKILETD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALQNENSHLGEQVQSAHQALSDIEERKKQHMFASSSSRVKEEILVQEKSALVSDLASLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESLKTNLENQNKRFDALTTENQSLRRANSELQEQSKIASEQ-----LSIAKDQI----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESVSSNQSSMNPIINGQIASN-SETKESTKASEASPSASSSVSSWSFLSSAKNALISLRD
                                                                                                                                                                                                                                                                                                                                    SQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQANQEEIMQKLTASISKAPQFGYP
                                                                                                                                                                                                                                                                                                                                                                  TLSEQIKNLESELNSSKIKNESLLNERNLLKEMLATSRSSILSHNSSAGNIDDKMKSIDE
                                                                                                                                                                                                                                                                                                                                                                                            SSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADA
                                                                                                                                                                                                                                                                                                                                                                                                                         TASETLVNKELANFSSIKEAVSKTLELREKVRALECDVEIQKQTVQYQISNAVKE---NSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QEACYLQLTASRTQCSDLSREVICLMAELDHLNETKSRNVPATVQVALDEYAQ----NPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNPATAKELQAMEAQLTAMSDQLVGADGEL-----PAEIQAIKDALAQALKQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIYMNFLSES------LETSNNN-----LTKVQAELLSTKMR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PEFSFTKVYSDNMKLQQKVSSLKLQLDRLTNKFSSFCEQVKQRIPVVKQQRSEIVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSPDNIAATKELID--AAETKVNELKQEHTGLTD--SPLVKKAEEQISQAQKDIQEIKPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTSIKELEEEVETQKRLTALWE-SKSSELQSEVAALQEKLTSQQSLYNNVTEELNNNKQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------DGLATAMGQVAFAAAKVGGGSAGT---AGTVQMNVKQLYKTAFSST
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1601
1727
               Zealand
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                                                                                                                                                                                                                                                      KYQQQLSTDRLTN----ANNDVEAFKKEAKELRSINQNLQDIIS
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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1664
              white;
                                                                               us (Rabbit).
Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%;
[F]
,
                                                                     Lagomorpha;
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                                                                                                                                                                                                                                                                                                             ---KNYEVYRNEMTAIQESLSKRNQDLLSEMEA-IRK-----
Roesch-Kleinkauf A.,
             TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 192.5;
Pred. No. 0.7
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COILED COIL (POTENTIAL).
MW; F820BF8D9C132644 CRC
                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                     Leporidae;
                                                                                                                                                                                   1938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .73;
                                                                                                                                                                                 AΑ
                                                                      Oryctolagus
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 Schuster
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 Η.,
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 Gasperik J.,
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ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00063; myosin_head; 1. Pfam; PF00612; IQ; 2. Pfam; PF01576; Myosin_tail; 1. Pfam; PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILES COILS.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED GREEDAMENT (C2).
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SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
  IIKDLERQNISYEAVLTNAGEVIKASSEAGIK----
                                            QLQVQAEADSLADAEERCDQLIKTKIQLEA--KIKEVTERAEDEEEINAELTAKKRKLED
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                                                                                                                                           KEMANMKEEFEKTKESLAKAEAKEKELEEKMVALM---
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ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (MONO-) (BY SIMILARITY).
METHYLATION (TRI-) (BY SIMILARITY).
METHYLATION (TRI-) (BY SIMILARITY).
ALKYLATION (SH-1) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
ALKYLATION (SH-2) (BY SIMILARITY).
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IQ.
COILED COIL (POTENTIAL).
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01-MAY-1991
                                                                                                                                                          Donelson J.E., Duke B.O.L., Moser D., Zeng W., Erond Lucius R., Renz A., Karam M., Flores G.Z.; "Construction of Onchocerca volvulus cDNA libraries characterization of the cDNA for a major antigen."; Mol. Biochem. Parasitol. 31:241-250(1988).
-i- FUNCTION: MAY BE A MYOFIBRILLAR PROTEIN.
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01-NOV-1995 (Rel.
30-MAY-2000 (Rel.
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                              modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                               "Molecular cloning of a gene expressed during development in Onchocerca volvulus."; Mol. Biochem. Parasitol. 69:161-171(1995).
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Coiled coil.
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000 (Rel. 39, Last sequence update)
001 (Rel. 40, Last annotation updat recognition protein (Natural-kille
                                                                                                                                                           EFVDG-ERSLAESQENAFRKO
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                                                                                                                                                                                  -EARKYEI-NDLQSRLDNAEQYLVTLQQNYVAVENERDMLYDALRRLHSMIDRT
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                                                                      STANDARD;
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B7132AACF1520317 CRC64;
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       cyclophilin-
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Best Local Sim
Matches 137;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L04288; AAA35734.2; -. EMBL; AF184110; AAD56402.1; - PIR; A47328; A47328. HSSP; Q27450; 1A33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93133824; PubMed=8421688; Anderson S.K., Gallinger S., Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Blood;
MEDLINE=93133824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A cyclophilin-related killer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ortaldo J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        related protein) (NK-TR
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PRINTS; PR0015
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NLKREHTKKVKEKLKGKKDKKHKAPKRKQAFHWQPPLEFGEEEEEEIDDKQVTQESKEKK
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                                       ---TEEVNNIKKALEAQKDTIDKL----
                                                                                   EIHIKVKPTTKSSTNTSLPDDNGAWKSSKQRTSTSDSEGSCSNSENNRGKPQKHKHGSKE
                                                                                                                          RVAAKDYDEAKSNEDTAKSGLENAKTLAEYETKMADLMAALQDMERLANSDPSNNH----
                                                                                                                                                                      RNGSKPKRKNYAGSKWDSESNSE-----RDVTKNSKNDSHPSSDKEEGEATSDSESEVS
                                                                                                                                                                                                             -----ASSSVSSWSFLSSAKNALISLRDAILN-KNSS-PTDSLSQLEA-STSTSTVT
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ARG/LYS-RICH (BASIC).
ARG/LYS-RICH (BASIC).
ARG/SER-RICH.
ARG/SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                                                                                                                                                                       Score 190.5;
Pred. No. 0.72
99; Mismatches
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ARG-SER TANDEM REPEAT-RICH.
MW; D98A1147763EF527 CRC64;
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RESULT NEW MELLING NEW MELLING
MYHL HUMAN.
P12882; Q9Y622;
01-OCT-1989 (Rel. 12, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, skeletal muscle, adult 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99318869; PubMed-10388558; Weiss A., Schiaffino S., Leinwand L.A.; "Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity.";
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TISSUE-Skeletal mu
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NTEENVACLQNIQHVEESVPNGVEDVLQTDDNMEICTPDR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNN---SPDNIAATKELIDAAETKVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTE-----VLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNAGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKQEHTGLTDSP---LVKKAEEQISQAQKDIQEIKPSGSDIPIVG-----PSGSAASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSPAKVEE
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851

KEMANMKEEFEKTKE - - ELAKTEAKRKELEEKMVTLM -

102 KDYDEAKSNFDTAKSGLENAKTLA---EYETKMADLMAALQDMERLANSDPSNNHTEEVN 158

Similarity

105;

Mismatches

Indels

140;

Gaps

24;

-QEKN

889

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Query Match
Best Local S
Matches 121
                                             CONFLICT
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CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                PRINTS: PR00193; MYOSINHEAVY.
ProDom: PD000355; myosin_head;
SMART: SM00015; IQ; 1.
SMART: SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF111785; AAD29951.1; -.
EMBL; X03740; CAA27380.1; -.
PIR; A23767; A23767.
HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb·sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02736;
                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 160730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                        NP_BIND
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                      Calmodulin-binding;
                                                                                                                                                                                                                                                                                                               Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                                                       PROSITE; PS50096;
                                                                                                                                                                                                                                                                                                                                                                                         Pram;
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                 PF01576;
                                                                                                                                                                                                                                                                                                                                                                                         PF00612;
                                                                                                                                                                                                                                                                                                                                                                                                  pF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGNC:7567; MYH1.
                                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                           IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000048; IQ_region.
IPR004009; Myosin_N.
IPR002928; Myosin_tail
                                                                                                                                                   1131
1139
1158
1163
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1302
                                    1470
1473
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1598
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1604
1648
1750
1822
1845
                                                                                                                                           145
                                                                                                                                                                                                                                      659
761
                                                                                                                                                                                                                                                                                                                                                                     Myosin_N;
                                                                                                                                                                                                                                                                                                                                                                                Myosin_tail; 1.
                                    Ą,
                                                       10; 1.
                                                                                                                                                                                                                                                                                                     ATP-binding; Methylation; Alkylation;
        5.9%;
                                    223114
                                                                                                                                                                                                                                                                                                               Coiled coil; Thick filament; Actin-binding;
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TESG -> Unu
VS -> ET (IN REF. 2).
R -> T (IN REF. 2).
E -> V (IN REF. 2).
AS -> SF (IN REF. 2).
" (IN REF. 2).
" FF. 2).
                                    ME RRORRE
                                                                                                                                                  A -> T (IN REF.
Q -> L (IN REF.
G -> V (IN REF.
A -> T (IN REF.
TESG -> QNQV (IN
VS -> ET (IN REF
       Score 190;
Pred. No. 1
                                                                                                                                                                                                          ALKYLATION
ALKYLATION
                                                                                                                                                                                                                                      ACTIN-BINDING ACTIN-BINDING
                                                                                                                                                                                                                            METHYLATION (TRI-) (POTENTIAL)
                                                                                                                                                                                                                                                        ATP (POTENTIAL)
                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                    MYOSIN HEAD-LIKE
                                    39ADB26AB79DFA53
                                                                (IN REF.
(IN REF.
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(IN REF.
(IN REF.
                                                                                                                                                                                                          (SH-1) (POTENTIAL)
(SH-2) (POTENTIAL)
         .1;
                                                                                                                                                                                                                                      (BY SIMILARITY).
                 1;
                Length 1939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEAD
                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN.
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RESULT 24
MYSD_CAEEL
                                                                                                                                                      MEDLINE-832/3000; running from the Caenorhabditis elegans "Rarn J., Brenner S., Barnett L.;
"Protein structural domains in the Caenorhabditis elegans "protein structural domains in the Caeno
                                                                    "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYSD_CAEEL STANDARD; PRT; 1938 AA. P02567; Q19674; 21-JUL-1986 (Rel. 01, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) MYO-1 OR R06C7.10.
                                                                                                                                                                                                                                                                                                                                                         Dibb N.J., Maruyama I.N., Krause M., Karn J.; "Sequence analysis of the complete Caenorhabditis heavy chain gene family."; heavy chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1256
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SEQUENCE FROM N.A.
                                                                                                              SEQUENCE OF 115-365 AND 1492-1763 MEDLINE-85201409; PubMed-3888374;
                                                                                                                                                                                                                                                                         SEQUENCE OF 34-1795 FROM N.A. MEDLINE-83273600; PubMed-6576334;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Bristol N2;
MEDLINE-89178677; PubMed-2926820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                            Cell Muscle Motil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483
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                                                                                                                                                                                                                                                                                                                                              Mol. Biol.
                                            ning nematode myosin genes.";
Muscle Motil. 6:185-237(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDQLSEIKTKEEEQQRLINDLTAQRARLQTESGEYSRQLDEKDTLVSQLSRGKQAFTQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S--DLSRELEEISERLEEAGG---ATSAQIEMNKKREAEFQKMRRDLEEATLQHEATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQEAHQQTLDD------LQAEEDKVNTLTKAKI-----KLEQQVDDLEGSLEQE 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLQLQVQAEADSLADAEERCDQLIKTKIQLEA--KIKEVTERAEDEEEINAELTAKKRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEELKRQLEEEI-KAKSALAHALQSSRHDCDLLREQYEEE----QEAKAELQ 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRKKHADSVAELGEQIDNLQRVKQKLEKEKSEMKMEIDDLASNMETVSKAKGNLEKMCRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSSSYA----AALSDGYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGLQSKIE-----DEQALGMQLQKKIKELQARIEELEEEIEAERASRAKAEKQR 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQP 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKIRMDL-----ERAKRKLEGDLKLAQESAM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAI-----AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDECSELKKDIDDLELTLAKV-EKEKHATENKVKNLTEEMAGLDETIAKLT----KEKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQIIKDLERQNISYEAVLTNAGEVIKASSEAGIK-----LGQALQSIVDAGDQSQAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ASQRAAETIVRD-----SQTLGDVYSR-LQVLDSLMSTIVSNPQA---N
                                                                                                                                                                                                                                                                                                                                           205:603-613(1989).
                                                                                                                                        FROM N.A.
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    CONFLICT
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EMBL;
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pfam; PF01576; Myosin_tail; 1.
pfam; PF02736; Myosin_t; 1.
prINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000355; myo: SMART; SM00242; MYSc;
                       CONFLICT
                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Multigene family.
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RRANGE REPORTED TO THE REPORT OF THE THE REPORT OF THE REP

846 1171 846 1170 660 764 128 700 710 710 389 391

METHYLATION ALKYLATION

ALKYLATION F -> E (IN | A -> R (IN | V -> D (IN |

HYLATION (TRI-).

YLATION (SH-1).

YLATION (SH-2).

> E (IN REF 2).

> R (IN REF 2).

> G (IN REF 4).

> D (IN REF 4).

> D (IN REF 2).

> O (IN REF 4).

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COILED COIL (POTENTIAL)

ACTIN-BINDING. ATP (BY SIMILARITY). LIGHT MEROMYOSIN (LMM)

ACTIN-BINDING.

RODLIKE TAIL (S2 AND LMM DOMAINS). ALPHA-HELICAL TAILPIECE (SHORT S2)

TAILPIECE (SHORT

MYOSIN HEAD-LIKE

myosin_head;

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RA Gardner A., McMuiray A.;

RI Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: MUSCLE CONTRACTION.

C -!- SUBBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C -!- SUBBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C -!- SUBCELLULAR LOCATION: THACK FILAMENTS (MLC-2).

C -!- SUBCELLULAR LOCATION: ThACK FILAMENTS (MLC-2).

C -!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARRYNGEAL MUSCLE.

C -!- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARRYNGEAL MUSCLE.

C -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

C CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

C -!- MISCELLANGEOUS: EACH MYOSIN THE SI DOMAIN ARE SELECTIVELY

ALKYLATED AND ARE REGUIRED FOR MYOSIN ATPASE ACTIVITY

ALKYLATED AND ARE REGUIRED FOR MYOSIN ATPASE ACTIVITY

MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED

C SUBERBACKENT (S2)
WormPep; P08799; 1MND.
WormPep; R06C7.10; CE06253.
InterPro; IPR004009; Myosin_tail.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as lower modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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S02772; MWKW1
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Z71266;
Z71261;
Z71261;
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CAA95806.1;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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Pred. No. 1.1;
17; Mismatches
                           Craniata; Vertebrata; Catarrhini; Hominidae;
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           CHARACTERIZATION.

MEDLINE-98437347; PubMed-9763420;

MEDLINE-98437347; PubMed-9763420;

Chan G.K.T., Schaar B.T., Yen T.J.;

Chan G.K.T., Schaar B.T., Yen T.J.;

Chan G.K.T., Schaar B.T., Yen T.J.;

"Characterization of the kinetochore binding domain of CENP-E

"Interactions with the kinetochore proteins CENP-F and hBUBR1."

"Interactions with the kinetochore proteins CENP-F and hBUBR1."

"Interactions with the kinetochore proteins CENP-F and BUBR1."

"Interactions with the kinetochore proteins CENP-E AND BUBR1."

"Interactions with the kinetochore proteins CENP-E AND BUBR1."

"Interactions with the kinetochore proteins GENP-E

"Interactions with the kinetochore proteins CENP-E

"Interactions with history proteins of CENP-E

"Interactions with the kinetochore proteins CENP-E

"Inte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95336446; PubMed-7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., C., Novel Cell-cycle-dependent 350-KDa nuclear protein: domain sufficient for nuclear localization.";
Biochem. Blophys. Res. Commun. 212:220-228(1995).
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Liao H., Winkfein R.J., Mack G., Rattner J.B., Y
"CENP-F is a protein of the nuclear matrix that
kinetochores at late G2 and is rapidly degraded
J. Cell Biol. 130:507-518(1995).
                           REPEAT
DOMAIN
                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                            EMBL; U19769; AAA82889.1; -. EMBL; U30872; AAA82935.1; -. EMBL; U25725; AAA86889.1; -.
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P34487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Futton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U1-FEB-1994 (Rel. 28, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 96.6 kDa protein F59B2.12 in chromosome
F59B2.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z11505; CAA77581.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S31132;
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   273
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                                                                                                                                                                                                                                                                                                                      HHHHHMESGPESVSSNQSSMNPI-INGQ-IASNSETKE----STKASEASPSASSSVSSW 56
NNSPDNIAA----TKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKP
                                                                                                                                                                                   GLE-NAKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLN 175
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                                   AASDAHSNFESLDAQGNKKSQNYSKKAASASGSNADFESNLESLKNADGTSMSNSTGNFN
                                                                  SADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQ
                                                                                                  EFVNQQNADGTFLRNNTGHKNTDEHLSHNVLDENAQMSIGADGTSHNITNRKGSVGDSHN
                                                                                                                               KLVTLQNQNKSL---TEVLKTTDS--ADQIPAINSQLEI-----
                                                                                                                                                                   GLEKSSKTYAD
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                                                                                                                                                                                                                                                                                                  HKGHHQSSGS---SSNTHSLTVVGADGKNITENSEKKDGYNKESKVDEANENTKIKSADG
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                                                                                                                                                                                                                                                                                                                                                                                                                              918 AA;
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-- 12; CE01024.
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                                                                                                                                                                                                                                                                                                                                                                                                                              96560 MW;
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20.2%;
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Pred. No. 0.49
15; Mismatches
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Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _YEAST
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical 99.7 kDa protein in SDL1
                                                         Hypothetical SIGNAL
                                DOMAIN
                                                                                   InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR000727; T_SNARE.
PROSITE; PS50192; T_SNARE; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIL169C OR YI9402.07C
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P40442;
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154
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POTENTIAL.
HYPOTHETICAL PROTEIN YIL169C.
T-SNARE COILED-COIL HOMOLOGY (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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VY-SRLQVLDSLMSTIVS
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VYTTTLDYVNATSTVVVS
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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MYSN_DROME STANDARD; PRT; 2017 AA.

ID MYSN_DROME STANDARD; PRT; 2017 AA.

AC Q99323;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin heavy chain, non-muscle (Zipper protein) (Myosin II).

EN ZIP.

OS Drosophila melanogaster (Fruit fly).
CE Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
RN [1]
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InterPro; IPR000048; IQ_region.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR CELLULARIZATION. REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORM; A LONG FORM (SHOWN HERE) A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcript: conserved sequences in the myosin tai splicing in the 5' untranslated sequence."; Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990).
                                                   1394
                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ketchum A.S., Stewart C.T., Stewart I "Complete sequence of the Drosophila
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TISSUE-Embryo;
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                                                                                                                              STKASEASPSASSSVSSWSFLSSAKNALISLRDAILNKNSSPTDSLSQLEASTSTSTVTR
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B36014; B36014.
                                                                           VAAKDYDEAKSNFDTAKSGLENAKTLAEYETKMADLMAALQDMERLANSDPS
                                                                                                     TNQLEEAELKASAAVKSASNMESQLTEAQQLLEEETRQKLGLSSKLRQIE---SEKEALQ
KKRLNKDIEALERQVKELIAQNDRLDKSKKKIQSELEDATIELEAQRTKVLELEKKQKNF
                        ----NNHTEEVNNIKKALEAQKDTIDKLNK------LVTLQNQNKSLTEVLKTTDSA
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PF00612; IQ; 1.
PF01376; Myosin_tail; 1.
PF02736; Myosin_t, 1.
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21.5%;
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Pred.
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MISSING (IN SHORT ISOFORM).
MW; 73E3CB02BA8F2528 CRC64;
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25 KDA/50 KDA JUNCTION.
50 KDA/20 KDA JUNCTION.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                REACTIVE SULFHYDRYL/ACTIN-BINDING LIGHT MEROMYOSIN (LMM).
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COILED COIL (POTENTIAL)
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tail and differential
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                                                                                                                                                               MEDLINE=90299827; PubMed=1694526; Goldschmidt R.M., Thoren-Gordon M., Cur Regions of the Streptococcus sobrinus determinants of antigen I.", J. Bacteriol. 172:3988-4001(1990).
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01-AUG-1991 (Rel. 19, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                -!- MISCELLANEOUS: IMMUNODOMINANT DETERMINANTS ARE LC C-TERMINAL TWO-THIRDS OF THE SPAA PROTEIN.
-!- SIMILARITY: BELONGS TO THE SPAP/SSP5/SPAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        Lapolla R.J., Haron J.A., Kelly C.G., Taylor W.R., Bohart Hendricks M., Pyati J., Graff R.T., Ma J.K.C., Lehner T.; "Sequence and structural analysis of surface protein antic (SpaA) of Streptococcus sobrinus."; Infect. Immun. 59:2677-2685(1991).
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STRAIN-6715 / Serotype G;
MEDLINE-91310320; PubMed-1855987;
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MISCELLANEOUS: IMMUNODOMIN
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 FGDKAGWTTTVSNG---
                        ----PALSRSVSRSGIESQGRSADASQRAAETIVRDSQTLGDVYSRL-----QVLDSL
                                                                                 QLYKTAFSSTSSSYAAALSDGYSAYK------TLNSLYSESRSGVQSAISQTAN
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AMIDE-LINKED TO CELL WALL (POTENTIAL).
A -> E (IN REF. 2).
Q -> K (IN REF. 2).
Q -> K (IN REF. 2).
A -> S (IN REF. 2).
A -> S (IN REF. 2).
- AEVKFASVLLKRGQSATATYTNLKNSYYNGKKISKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL SURFACE ANTIGEN I.
CELL SURFACE ANTIGEN II.
REMOVED BY SORTASE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B235F9CCD92838E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1528;
                                                                                                           -GNLSEPSAQSLVYDLE
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RESULT 30
MYSS_CYPCA
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This SWISS-PROT entry is copyright. It is produced through a clothern the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
-!- CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERRISTIC FOR ALPHA-HELICAL COLLED COILS.
-!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watabe S., Imai J., Nakaya M., Hirayama Y., Okamoto Y., Masa Uozumi T., Hirono I., Aoki T.; "Temperature acclimation induces light meromyosin isoforms w different primary structures in carp fast skeletal muscle."; Biochem. Biophys. Res. Commun. 208:118-125(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirayama Y., Watabe S.; "Structural differences in the crossbridge head of temperature-"Structural differences in the crossbridge head of temperature-
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Myosin heavy chain, fast skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97176447; PubMed=9023993;
Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
"CDNA cloning of myosin heavy chain isoforms from carp fast skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fast muscle;
MEDLINE=97352533; PubMed=9208928;
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                                                                                                                                                          SUBFRAGMENT (S2).
SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
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tent is in no
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pram; PF01576;
Pfam; PF02736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00193; MYOSINHEAVY
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                                                                 QLTAMSDQLVGADGELPAEIQAIKDALAQALKQ--PSADGLATAMGQVAFAAAKVGGGSA
                                                                                                             SAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEA 403
                                                                                                                                                   ELIDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAA
                                                                                                                                                                                AQESIMDLENEKQQSDEKIKKKDFEISQLLSKIED--EQSLGAQLQKK-----IK 1110
                                                                                                                                                                                                                               Q-----AEEDKVNTLTKAKTKLEQQVDDLEGSLEQEK----KLRMDLERAKRKLEGDLKL
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D50476; BAA09
D43700; BAA07
P13538; 2MYS.
                      GTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKT-----LNSLYSESRSGVQ
                                              DSVA---
                                                                                                                                      EL----QARIEELEEEIE--AERAARAKVEKQRADLSRELEEI--
                                                                                                                                                                                                                                                     NKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTN 234
                                                                                                                                                                                                                                                                           KKDIDDLELTLAKVEKEKHATENKVKNLTEEMASQDESIAKLTKEKKALQEAHQQTLDDL
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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IPR004009; Myosin_N.
IPR002928; Myosin_tail
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 ·NLEKMCRT - - -
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Myosin_N; 1.
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                                           -GEQIDNLQRVKQKLEKEKSEYKMEIDDLTSNMEAVAKAKA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 187.5;
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED COIL (POT ATP (POTENTIAL). ACTIN-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coil; Thick filament; Actin-binding;
lation; Calmodulin-binding;
                                                                                       NKKREAEFQKMRRDLEESTLQHEATAAALRKEQA
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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 -LEDQLSEIKTKSDENVRQLNDM----
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This SWI between

EMBL; X05958; CAA29391.1; PIR; A02985; A02985. PIR; A05280; A05280.

S00084

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                                                                                                                                                                                                                                                                                                                                                           Maeda K., Sczakiel G., Wittinghofer A.;

"Characterization of cDNA coding for the complete light meromyosin portion of a rabbit fast skeletal muscle myosin heavy chain.";

Eur. J. Biochem. 167:97-102(1987).

-i- FUNCTION: MUSCLE CONTRACTION.

-i- SUBUNIT: MUSCLE CONTRACTION.

-i- SUBUNIT: MUSCLE WYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF HEAVY CHAIN SUBUNITS (MHC). 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-258.
Capony J.-P., Elzinga M.,
"The amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Myosin heavy chain, skeletal muscle (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region in myosin subfragment 2.";
J. Biol. Chem. 260:3456-3461(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87304245; PubMed=3305014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 409-1084 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The amino acid sequence and stability region in myosin subfragment 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=85131142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 259-428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biophys. J. 33:148A-148A(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.C., Wong A.
                                                                                                                                                                                                                                                                DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM), IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                    SUBFRAGMENT (S2).
SIMILARITY: THE P
WHICH DICTATE THE
                                                                                                                                SWISS-PROT entry is copyright. It is produce een the Swiss Institute of Bioinformatics and remarked institute. There are
                                                                                                                                                                                                          CONSERVED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LODAEE-SIEAVNSKCASLEKTKORLOGEVEDLMIDVERANSLA---ANLDKKORNF 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRDSQTLGDVYSRLQVLDSLMSTIVS -- NPQANQ ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RARLQTENGEFSRQLEEKEALVSQLTRGKQAYTQQIEELKRHIEEEEVKAKNALAHAVQSA 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAISQTANPALSRSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHDCDLLREQYEEEQEAKAELQRGMSKANSEVAQWRTKYETDAIQRTEELEEAKKKLAQR 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISKAPQFGYPAVQNSADSLQKFAAQLERE----FVDGER--SLAESQENAFRKQPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                    THE PERIODICITIES OF THE ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=3972832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us (Rabbit).
Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ⊠
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Best Local Sin
Matches 145;
  MYH7_PIG
P79293;
15-DEC-1998
15-DEC-1998
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ATP-binding; Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                               AGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAET----KVNELKQEHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALQDMERLANSDPSNNHTEEVNNI-------KKAL-EAQKDTIDKLNKLVTLQNQN 184
                                                                                             RLQNEAEDLMIDVERSNA
                                                                                                                      QLERE----FVDGERSLA 630
                                                                                                                                            MSKANSEVSQWRTKCETDAIQRTEELEEAKKKLAQRLQDAEEH-VEAVNSKCASLEKTKQ
                                                                                                                                                                    VS--NPQANQ-----
                                                                                                                                                                                                                   VSRSG--
                                                                                                                                                                                                                                                                                                                                                 SLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPA
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                                                                                                                                                                                                                                                                                                                                                                                 AERASR--AKAEKQRSDLSRELEEI-----SERLEEAGGA-----TSAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVNTLTKAKTKLEQQVDDLEGSLEQEK----KIRMDLER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMANMKEEFEKTKESLAKAEAKRKE-----LEEKMVALMQEKNDLQLQVQAEADSLADAE
                                                                                                                                                                                         LSRGGQAFTQQIEGLKRQLEEETKAKSALAHALQSSRRDCDLLREQYEEEQEAKAELQRA
                                                                                                                                                                                                                                                              SSTSSSSYAAALSDGYSAYKTLNSLYSE--SRSGVQSAISQTANPALSR-----S
                                                                                                                                                                                                                                                                                       NLQRVKQKLEKEKSELKMEIDDLA-----
                                                                                                                                                                                                                                                                                                           EIQAIKDALAQALKQ--PSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAF
                                                                                                                                                                                                                                                                                                                                                                                                       GLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRI
                                                                                                                                                                                                                                                                                                                                                                                                                               GDLKLAQ--ETSMDIENDKQQLDEKLKKLEFMINLQSKIEDEQALMINLQRIEELEEEIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAKVEKEKHATENKVKNLTEEMAGLDETIAKLTKEKKALQEAHQQTLDDLQ-----AEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERQDLIKTKIQLEAKIKEVT---ERAEDEEEINAELTAKKRKLEDECSELKKDIDDLELT 118
                                                                                                                                                                                                                                       -----LEDQLSEVKTKEEEHQRLINELSAQKARLHTESGEFSRQLDEKDAMVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QLEASTSTSTVTRVAAKDYDEAKSNFDTAKSGLENAKTLAEYETKMADLM 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258
258
258
455
405
408
421
(Rel. 37, Created)
(Rel. 37, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                    -NKKREAEFEKMRRDLEEATLQHEATAAALRKKHADSVA---EL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                      STANDARD;
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259
1084
1084
405
408
421
423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%;
                                                                                              586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED COIL (POTENTIAL).
L -> V.
V -> L.
E -> D.
S -> G.
K -> R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.69
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 187;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RODLIKE TAIL (S2 AND LMM DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-HELICAL TAILPIECE
                                      PRT;
                                                                                                                                                                  EEIMQKLTASISKAPQFGYPAVQNSADSLQKFAA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229CFD69A6E1F7F0 CRC64
                                      1935 AA.
                                                                                                                                                                                                                                                                                       ·----GNMETVSKAKGNLEKMCRT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AKRKLE
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                                                                                                                                                                                                                                                                                                                                    GEQID
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Query Match
Best Local
                                                                                         MOD_RES
MOD_RES
                                                                                                                                                             NP_BIND
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

OMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWN CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEL CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

OHMARIN: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 IMPORTATION OF THE STREET OF THE STRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00015; IQ; 1. SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01576; Myosin_tail; 1. Pfam; PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBFRAGMENT (S2).
-!- MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: MUSCLE CONTRACTION.
-:- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS
-:- SUBUNIT: MUSCLE MYOSIN SA HEXAMERIC PROTEIN THAT CONSISTS
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                        Calmodulin-binding.
                                                                                                                                                                                                                                                                                                                              Myosin; Muscle protein; Co
ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U75316; AAB37320.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KO Y.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P08799; 1MND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001609; myosin_head.
                                                                                                                  781
839
178
655
757
129
695
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                                                                      ΑĄ,
                                                                                                                    810
1935
185
677
771
129
695
5.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiac muscle beta isoform (MyHC-beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin_tail
                                                                      223110
                                                                                                                                                                                                                                                                                                                              Coiled coil; Thick filament; Actin-binding;
n; Alkylation; Multigene family;
                                                                      MW;
  Score 187;
Pred. No. 1
                                                                                                                                                             COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                         METHYLATION (TRI-) (POTENTIAL) ALKYLATION (SH-1) (POTENTIAL). ALKYLATION (SH-2) (POTENTIAL).
                                                                                                                                                                                                                                                                               MYOSIN HEAD-LIKE
                                                                      149CDBFD910DBB08 CRC64;
                        DB
                        1:
                     Length 1935;
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MESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALI 67

Matches

Conservative

134;

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307;

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MAR binding
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                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. VFNT Cherry; TISSUE-Fruit;
STRAIN-CV. VFNT Cherry; TISSUE-Fruit;
MEDILINE-97112038; PubMed-8953774;
Meier I., Phelan T., Gruissem W., Spi
MEFI, a novel plant filament-like pr
                                                                             attachment region DNA.";
Plant Cell 8:2105-2115(1996).
-!- FUNCTION: BINDS DNA. INTE
                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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ARCHITECTURE BY
               FUNCTION: BINDS DNA. INTERACTS WITH CHROMATIN VIA MATRIX ATTACHMENT REGIONS (MARS). LIKELY TO PARTICIPATE IN NUCLEAR MARCHITECTURE BY CONNECTING CHROMATIN WITH THE NUCLEAR MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIE---
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filament-like protein 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein; DNA-binding; Coiled coil.

DOMAIN 125 681 COILED COIL (
DOMAIN 10 15 POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIALLY WITH THE NUCLEAR ENVELOPE. SUBCELLULAR LOCATION: NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVLEEKITLLTTEIKDKEVSLRSNTSKLAEKESEVNSLSDMYQQSQDQLMNLTSEIKELK 305
                                                                                                                                                                                                                                                     AAKGEILRLRSQINSVK
                                                                                                                                                                                                                                                                               GADGE---LPAEIQAIK 427
                                                                                                                                                                                                                                                                                                                                                                                        QEIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIAATKELIDAAETKV------NELKQEHTGLTDSPLVKKAEEQISQAQKDI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAKTLAEYETKMADLMAALQDMERLANSDPSNNH-----TEEVNNIKKALEAQKDTIDK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISL----RDAILNKNS---SPT
                                                                                                                                                                                                                                                                                                              SRNSSLEDEREVHRQSVSEQKQISQEAQENLEDAHSLVMKLGKERESLEKRAKKLEDEMA
                                                                                                                                                                                                                                                                                                                                         ----LQGFR-----SMIEQFNVNNPA-----
                                                                                                                                                                                                                                                                                                                                                                      KELRKSLED------ELEKATES-----LDEINRNVLALAEELELAT
                                                                                                                                                                                                                                                                                                                                                                                                                                ELVAVSENRDSLQTELVNVYKKREHTRNELKQEKT----IVRTLEEELKFLESQITRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDETKHSSELLAAELTTTKELLKKTNE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKQEIEVTQESLENSRSEVSDITVQLEQLRDLSSKLE---REVSKLQMELEETRASLQRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNK -- LYTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNISYE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDATLGEQEKRLHQ----LEEQLGTALSEASKNEVLIADLTREKENLRRMVDAELDNVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEIQKRERELELKCVSEDNLNVQLNSLLLERDESKKELHAIQKEYSEFKSNSD---EKVA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
98; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPD
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697 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.8%;
19.7%;
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79516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 186; DB
Pred. No. 0.44
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-SER.
; 700A56D68D6A7E49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151;
                                                                                                                                                                                                                                                                                                                                          -TAKELQAMEAQLTAMSDQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EMHTMSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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MYHB_HUMAN STANDARD; PRT; 1972 AA. P35749; 000396; P78422; 094944; 01-JUN-1994 (Rel. 29, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 18-OCT-2001 (Rel.

Homo sapiens (Human). Eukaryota; Metazoa; (Mammalia; Eutheria; F

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

(SMMHC)

MYH11 OR KIAA0866.

NCBI_TaxID=9606;

SEQUENCE

z

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AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-i- TISSUE SPECIFICITY: SMOOTH MUSCLE; EXPRESSED IN THE UMBLICAL ARTERY, BLADDER, ESOPHAGUS AND TRACHEA.
-i- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
-i- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-i- DISEASE: A chromosomal rearrangement, known as pericentric inversion Inv(16) (pl)3922), Produces a fusion protein that consists of the 165 N-terminal residues of CBF-beta (PEPB2) with the tail region of MYH11. This rearrangement is associated with acute
                                                                                                                                                                                                    between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entitles requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA sequence human chromosome 16p and 16q."; Genomics 60:295-308(1999).
                                                                                                                               EMBL;
                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93263189; PubMed-7684189;
Matsuoka R., Yoshida M.C., Furutani
Yanagisawa M., Masaki T., Takao A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; *Prediction of the coding sequences of unidentified human genes. XII The complete sequences of 100 new cDNA clones from brain which code the complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okajima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1093-1972 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human smooth muscle myosin heavy chain region 16q12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 885-1972 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99156230; PubMed-10048485,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-1266 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99425270; PubMed=10493829;
                                                         3enew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS ()
                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                        myeloid leukemia of M4EO subtype.
MISCELLANEOUS: EACH MYOSIN HEAVY KEROMYOSIN (HMM). IT CAN LATER BE
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                           SUBFRAGMENT (S2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              large proteins in vitro.";
                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                           P10587;
                                                                                          D10667; -; NOT_ANNOTATED_CDS X69292; CAA49154.1; -.
                                                                                                                               U91323; AAC35212.1; -. AB020673; BAA74889.1; -
                                                                                                                                                                 AF001548; AAC31665.1; -.
                                                     HGNC:7569; MYH11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5:355-364(1998).
IPR000048; IQ_region IPR004009; Myosin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genet.
                                                                           1BR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46:61-67(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Furutani Y.,
                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                       There
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                      Usage
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                                                                                                                                                                                                                                                                             restrictions
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                                                                                                                                                                                                                                                                                                a collaboration
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CONFLICT
CONFLICT
CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
SMART; SM00015; IO; 2.
SMART; SM00242; MYSC; 1.
1303
                                                                                              1188
                                                                                                                                           1129
                                                                                                                                                                                            1075
                                                                                                                                                                                                                                           1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02736;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00063; myosin_head; 1. Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
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                      494
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                                                                                                                                                                                                                                                                                                                                                                                                               111 FDTAKSGLENAKTLAEYETKMADLMAALQDMERLAN--SDPSNNH---TEEVNNIKKALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
AIKLAKDVASLSSQLQD-TQELLQEETRQKLNVSTKLRQLEEERNSLQDQLDEEMEAKQN 1361
                     GYSAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRS----ADASQRAAET
                                                                                                                                           SERAARNKAEKQKRDLGEELEALKTELED-TLDSTATQQELRAKREQEVTVLKKALDEET
                                                                                                                                                                    NEMAA------IALQGFRSMIEQFNVNNPATAKELQAM------
                                                                                                                                                                                            QAQIAELKMQ-----LAKKEEELQAALARLDDEIAQKNNALKKIRELEGHISDLQEDLD
                                                                                                                                                                                                                   QKDIQEIKPSGSDIPIVGPSGSAASAGSAA--GALKSSNNS-----
                                                                                                                                                                                                                                                                                          Q-LEEEEAARQKLQLEKVTAEAKIK--KLEDEILVMDDQNNKLSKERKLLEERISDLTIN
                                                                                                                                                                                                                                                                                                                 ONISYEAVLTNAGEVIKASSEAGIKLGOALQSIVDAGDQS-----QAAVLQAQQNNSPDN
                                                                                            RSHEAQVQEMRQKHAQAVEELTEQLEQFKRAKANLDKNKQTLEKENADLAGELRVLGQAK
                                                                                                                   ---EAQLTAMSDQLVGADGELPAEIQAIKDALA-----QALKQPSAD--GLATAMG---
                                                                                                                                                                                                                                           LAEEEEKAKNLTKLKNKHESMISELEVRLKKEEKSRQELEKLKRKLEGDASDFHEQIADL 1074
                                                                                                                                                                                                                                                                IAATKE-----LIDAAETKVNEL-----KQEHTGLTDSPLVKKAE-----
                                                                                                                                                                                                                                                                                                                                         AETELYAEAEEMRVRLAAKKQELEEILHEMEARLEEEEDRGQQLQAERKKMAQQMLDLEE
                                                                                                                                                                                                                                                                                                                                                             AQKDTIDKLNKL-VTLQNQNKSLTEVLKTTDS-ADQIPAINSQLEINKNSADQIIKDLER
                                                                                                                                                                                                                                                                                                                                                                                        FTKVKPLLQVTRQEEEMQAKEDELQKTKERQQKAENELKELEQKHSQLTEEKNLLQEQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002928; Myosin_tail.
IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  786
844
1935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701
711
887
1263
1558
1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178
661
762
129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                           -QVAFAAAKVGGGSAGTAGTVQMN--VKQLYKTAFSSTSSSSYAAALSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               815
1934
1972
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1558
1558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227338 MW; 67665BB2AECE1277 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TH:) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
EEK -> NSE (IN REF. 3).
ELQS -> TLSF (IN REF. 2).
T. > S (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 186; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQ -> NE (IN REF. 3)
A -> S (IN REF. 4).
T -> L (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED COIL (POTENTIAL).
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AKA9_RABIT
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Matches 139
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Q28628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein (AKAP120) from rabbit gastric parietal cells.", Biochem. J. 322:801-808(1997).
-i-FUNCTION: BIADS TO TYPE II REGULATORY SUBUNITS OF P. A. MAY BE A SCAFFOLDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seguence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
A-kinase anchor protein 9 (Protein kinase A anchoring
(PRKA9) (A-kinase anchor protein 120 kDa) (AKAP 120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97220389; PubMed=9148752;
Dransfield D.T., Yeh J.L., Bradford A.J., Goldenring J.R.;
"Identification and characterization of a novel A-kinase-anchoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=New Zealand white; TISSUE=Gastric parietal cell; MEDLINE=97220389; PubMed=9148752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN GASTRIC PARIETAL CE
DOMAIN: RII BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC
COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A
COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A
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  AATKELIDAAETKVNELKQEHTGLTDSPLVKK-AEEQISQAQKDIQEIKPSGSDI---PI
                                                                                                           TNAGEVIKAS-----SEAGIKLGQALQSI-----VDAGDQSQAAVLQAQQNNSPDN--I
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                                                        EKLGFAIKESDAVSPQDQQVLFGKFAQIIHEKEVEIDRLNE-QIIKLQQQLKITTDNKVI
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8; Mismatches
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Pred. No. 0.8;
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RESULT 36
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DE Chromod SMC C
OS Mycob
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SEQUENCE FROM N.A.
STRAIN-CDC 151 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.
Fleischmann R.D., Alland D., Eisen J.
Peterson J., DeBoy R., Dodson R., Gwi
Kolonay J.F., Nelson W.C., Umayam L.,
Delcher A., Utterback T., Weidman J.,
Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMC_MYC
                                                                                                                                                                                                                                                 MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentlee S., Hamilin N., Holroy,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Phylogenetic analysis of SMC proteins."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H37Rv;
Cobbe N., Hec
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
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                             ., Eisen J.A., Carpenter L., White O., Son R., Gwinn M.L., Haft D., Hickey E. Umayam L.A., Ermolaeva M.D., Salzberg Weldman J., Khouri H., Gill J., Mikula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN CHROMOSOME STRUCTURE PARTITIONING. ESSENTIAL FOR CHROMOSOME PARTITION (BY SIMI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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EIDKARSELAAAEALAAQLNAALAGALTEQSARQDAAEQALAALNESDTAISAMYEQLGR
                                                                                                                    VLSDWPAPQAPQSASGEMLPSGAQWALDLVE----SPPQLVGAMIAMLSGVAVVND-LTE
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                          QLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAI--SQTANPALSRSVSR
                                                                         ADG--ELPAEIQAIKDALAQALKOPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVK
                                                                                                                                               LLDD------VDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVG
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Pred. No. 0.91;
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Pfam; PF01302; CAP_GLY; 2.
SMART; SM00343; ZnF_C2HC; 1.
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PROSITE; PS50245; CAP_GLY_2;

InterPro; IPR000938; CAP-Gly.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bilbe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W., de Wolf-Peeters C., Shipman R.; "Restin: a novel intermediate filament-associated protein highly expressed in the Reed-Sternberg cells of Hodgkin's disease."; EMBO J. 11:2103-2113(1992).
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-
Sternberg intermediate filament associated protein).
                                                                                                                                                                                                                                                                      EMBL; X64838; CAA46050.1; EMBL; M97501; AAA35693.1;
                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG OF HODGKIN'S DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE CYTOSKELETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92405160; PubMed=1356075; Pierre P., Scheel J., Rickard J.E., "CLIP-170 links endocytic vesicles t Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Peripheral blood monocytes; MEDLINE=92289675; PubMed=1600942;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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to microtubules.";
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RESULT 38
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CONFLICT
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DOMAIN 7
DOMAIN 14
DOMAIN 23
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DOMAIN
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01-OCT-1989
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                    Myosin
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                                                              MYSC_CAEEL
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                                                                                                          QFNMLSSDLEKLR----ENLADMEAKFREKDERE
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                                                                                                                                                                                                                                                                 MAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALA
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                                                                                                                                            LKLTNLQENLSEVSQ-VKETLEKELQILKEKFAEASEEAVSVQRSMQETV--NKLHQKEE
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3
                    heavy
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                 (Rel. 12, L
9 (Rel. 12, L
J1 (Rel. 40, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1069
7 AA;
                                                               STANDARD;
                                                                                                                                                            ADASQRAAETIVRDSQTLGDVYSR-----LQVLDSLMSTIVSNPQANQEE
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                    (MHC
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Last sequence up
Last annotation
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                    <u>C</u>
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COILED COIL
CCHC-BOX.
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CAP-GLY 2.
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Pred. No. 1.1
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D -> E (IN REF. 2).
WW; 0A4F166DD94254E8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1427;
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            DOMAIN
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CONFLICT
                                                                                                Myosin; Muscl
ATP-binding;
                                                                                                                 ProDom; PD000355; myos
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditidae;
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            856
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174
668
773
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718
                                                                                                 Methylation;
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EMBL; X08066; CAA30855.1;
EMBL; M37233; AAA28122.1;
EMBL; M37235; AAA28122.1;
EMBL; M37236; AAA28123.1;
PIR; S05697; S05697
HSSP; P10587; 1BR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dibb N.J., Maruyama I.N., Krause M., "Sequence analysis of the complete Cheavy chain gene family.";
pfam; PF00063; myosin_head; 1.
pfam; PF01576; myosin_tail; 1.
pfam; PF02776; myosin_t; 1.
pfam; PF02778; myosin_t; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformat,
the European Bioinformatics Institute. The
use by non-profit institutions as long a
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning nematode myosin genes."; Cell Muscle Motil. 6:185-237(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2; MEDLINE=89178677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                    InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                entities requires a or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=85201409; PubMed=3888374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Karn J., Dibb N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MCC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MCC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARYNGEAL MUSCLE.

TOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDE
CCHARACTERISTIC FOR ALPHA-HELICAL COILED COLLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFRAGMENT (S2).
MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peloderinae;
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AAA28121.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLOBULAR HEAD DOMAIN
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MYSC; 1.
protein; Coiled coil; Thick filament; Actin-binding;

Alkylation; Multigene family.

L M M

myosin_head;

855 1947 1947 181 690 787 125 708

ALKYLATION ALKYLATION E -> D (IN

(SH-1). (SH-2). (REF. 2)

ACTIN-BINDING.
METHYLATION (TRI-) ATP (BY SIMILARITY). ACTIN-BINDING. RODLIKE TAIL (S2 AND LMM COILED COIL (POTENTIAL). MYOSIN HEAD-LIKE

(POTENTIAL)

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RESULT 39
YJH8_YEAST
ID YJH8_Y
AC P47033
DT 01-FEB
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YJH8_YEAST STANDARD;
P47033;
O1-FEB-1996 (Rel. 33, Created)
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Pred. No. 1.
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                                                 881
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)2-Cys6 binuclear cluster domain and a putative alpha 2-SCB-alpha 2 binding site."; Yeast 11:681-689(1995).

-i- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR000837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z49353; CAA89370.1; -.
EMBL; X83502; CAA58492.1; -.
EMBL; X8851; CAA61314.1; -.
HSSP; P04284; ICFE.
SGD; S0003614; YJL078C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96093911; PubMed=7483841;
Miosga T., Schaaff-Gerstenschlaeger I., Chalwatzis N.,
Boles E., Fournier C., Schmitt S., Velten C., Wilhelm P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33,
16-OCT-2001 (Rel. 40,
Hypothetical 89.2 kDa
YJL078C OR J1027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zimmermann F.K.; "Sequence analysis of a 33.1 kb fragment from the left arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288c;
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                                                                                                                                                     V-NTDVSVTSVSSTAHTTKDTATTSVTASESITSETAQASSSTE---
  IDAAETKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSGSAASA
                                                                YSNSASVSGHGVTYAAEVAITSEQSSALATSVPATNCSSIVKTTTLENSSTTTITAITKS
                                                                                                                                                                                                                                          SATNAAQYAT -----
                                                                                                                                                                                                                                                                                                                                                   RDAILN-----KNSSPTDSLSQLEASTSTSTVTRVAAKDYD-----EAKSNFDTAKSGLE
                                                                                                           LTNAGEV----IKASSEAGIKLGQ--ALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKEL
                                                                                                                                                                                             LQNQNKSLTEVLKT-----
                                                                                                                                                                                                                                                                                  NAKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVT
                                                                                                                                                                                                                                                                                                                                                                                                               SDPTSSTAAASSSDPASSSAAASSSASTENAASSSSAISSSSSMVSAPLSSTLTTSTASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       881 AA; 89152 MW;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                           -TDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAV
                                                                                                                                                                                                                                        RLGSSSRSSSGAVSSSAVSQSV-----LNSVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 184; DB 1;
Pred. No. 0.71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37DBAC660CA9D12A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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SCP160-SMC3 intergenic region
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MYH4_HMAN

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                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weiss A., Schiaffino S., Leinwand L.A.;

"Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity.";

J. Mol. Biol. 290:61-75(1999).

-!- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                    or send
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TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99318869; PubMed=10388558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                               SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSQTLGDVYSRLQ
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                                                                   AF111783; AAD29949.1; -.
HGNC: 7574;
                                                                                                                                 an email to license@isb-sib.ch).
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theria; Primates;
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Catarrhini; Hominidae;
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InterPro; IPR002928; Myosin_tail
InterPro; IPR001609; Myosin_head
Pfam; PF00063; Myosin_head; 1.
Pfam; PF00612; IQ; 2.
Pfam; PF00576; Myosin_tail; 1.
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SEQUENCE
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SMART; SM00242; MYSC;
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PRINTS; PR00193; MYOSINHEAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEMANMKEEFEKTKE--ELAKTEAKRKELEEKMVTLM-----
                                                                                 VLD--SLMSTIVSNPQANQEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFV
                                                                                                                                                                                                                                                                                                    KKLCMDL-----ERAKRKLEGDLKLAQESTM-----DTENDKQQLNEKLKKKEFEM 1091
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EFSRQLDEKDAMVSQLSRGKQAFTQQI
                              DGERSLAESQ---ENAFRKQPAFIQQV 647
                                                            INDLASNMET-VSKAKANFEKMCRTLEDQLSEI-KTKEEEQQRLINELSAQKARLHTESG
                                                                                                                      KMRRDLEESTLQHEATAAALRKKHADSVAELGKQIDSLQRVKQKLEKEKSEL-----KME
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                                                                                                                                                                                EEISERLEEAGG --- ATSAQIELNKKR ---
                                                                                                                                                                                                            GOVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYS 506
                                                                                                                                                                                                                                           SNLQ--GKIEDEQALAMQLQKKIKELQARIEELEEEIEAERASRAKAEKQRS--DLSREL
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                                                                                                                                                                                                                                                                                                                                KPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQ
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C;Accession: G71490
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
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A; Gene: CT622
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A;Experimental source: serotype D, strain UW-3/Cx
C:Comment: This sequence was originally identified as homologous to part of a sequenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MESGPESVSSNQSSMNPIINGQIASNSETKESTKESEASPSASSSVSSWSFLSSAKHALI
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93.9%;
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Pred. No. 1.9e
15; Mismatches
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B90835
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T30336
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Gaps

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67

427 354 367 307 234 247

294

187

174

127 60

120

Result No.

Minimum

Searched:

Sequence:

9

Copyright

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5.1.4_p5_4578 Compugen Ltd.

Maximum

DB Bd

Database

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Conserved hypothetical protein CP0018 [imported] - Chlamydophila pneumoniae (strains CWL N;Alternate names: chlpn 76 kda homolog_1 (ct522); hypothetical protein CPn0728 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: D72042 p81623
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: D72042
A;Molecule type: DNA
A;Residues: 1-51 <ARN>
A;Residues: 1-51 <ARN>
A;Residues: 1-51 <ARN>
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Accession: D81623
A. (Textis: NoPn and Chlamydia pneumoniae AR39.
A;Accession: D81623
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A;Experimental source: strain AR39, HL cells
C;Comment: This sequence was originally identified as homologous to part of a sequence
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A; Gene: CPn
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A;Molecule type: DNA
A;Residues: 1-651 <REA>
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IAQSLVDQTDATATQIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK
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                                                                                                                 LNKLYTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNI---SYEA
                                                                                                                                                     TSLADIQAALVSLQDAVTNIKDTAATD-----EET----AIAAEWETKNADAVKVGAQ
                                                                                                                                                                                                                            NALMSLADKLGIASSNSSSSTSRS-ADVDSTTATAPTPPPPTFDDYKTQAQTAYDTIFTS
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                                                                                ITELAKYASDNQAILDSLGKLTSFDLLQAALLQSVANNNKAAELLKEMQDNPVVPGKTPA
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A;Molecule type: DNA
A;Residues: 1-651 <STO>
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                           IAQSLVDQTDATATQIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK
                                                      VLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAE
                                                                                                                       LNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNI---SYEA
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QKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQENAFRKQPAFIQQ
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                                                                                                    SVPRARTEARG-PEKTDQALARVISGNSRTLGDVYSQVSALQSVMQIIQSNPQANNEEIR
                                                                                                                              SVSRSGIESOGRSADASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQANQEEIM
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CHLPN 76 kDa homolog_1 (CT622) [imported] - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: E86581 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Sh Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349; PMID:10871362 A;Accession: E85581 A;Cross-references: GB:BA000008; NID:g8979100; A;Experimental source: strain J138 C;Genetics: A;Gene: CPj0728 Score 894; DB Pred. No. 8.3e 26; Mismatches DB 2; 3.3e-31; PIDN:BAA98935.1; Length 651; GSPDB:GN00142 shiba, J138)

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A;Residues: 1-715 <RES>
A;Residues: 1-715 <RES>
A;Cross references: GB:L23921; NID:g435961; PIDN:AAA23117.1; PID:g435962
A;Experimental source: strain AR-39
C;Comment: This is the hypothetical translation of a sequence that was reported
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Perez-Melgosa, M.; Kuo, C.
Infect. Immun. 62, 880-886, 1994
A;Title: Isolation and characterization of a gene encoding A;Reference number: 140729; MUID:94156481; PMID:7509320
A;Accession: I40729
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical 76K protein - Chlamydophila pneumoniae (strain AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 16-Aug-1996 *sequence_revision 16-Aug-1996 *text_change 31-Mar-2000
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TKVNELKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPS-GSDIPIVGPS-GSAASAGSA
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                                                                                              VLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAE
                                                                                                                                    ITELAKYASDNQAILDSLGKLTSFDLLQAALLQSVANNNKAAELLKEMQDNPVVPGKTPA
                                                                                                                                                                           LNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQNI---SYEA
                                                                                                                                                                                                                TSLADIQAALVSLQDAVTNIKDTAATD-----EET----AIAAEWETKNADAVKVGAQ
                                                                                                                                                                                                                                                       KTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTID-----K
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28.9%; Pred. No. 4.2e-12;
ative 94; Mismatches 193;
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A;Accession.
A;Katus: preliminary
A;Molecule type: DNA
A;Residues: 1-2271 <KUR>
A;Cross-references: GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149
A;Cross-references: GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149
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C; Date: 10-May-2001
C; Accession: F90073
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A;Title: Whole genome sequencing of meticilin-resistant Stapylococcus aur A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F90073
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bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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                                        ----IASLSTSVSTSESGS-----TSESTSESDSTSTSLSDSQSTSR-----
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  YSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQ---
                                                                                                                  TSTSLSNSASASE----SDSSSTSLSDSTSASMQSSESDSQSTSASLSDSLSTSTSNRMST
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                                                                           AMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSL
                                                                                                                                                     EQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLAT
                                                                                                                                                                                                                                 EIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMI 384
                                                                                                                                                                                                                                                                                                                PDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQI------SQAQKDIQ
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20.6%; Pred. No. (
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Sekimizu,
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÷1	Qy 428 DALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSY 487 : : : : : : :	Qy 393 ATAKELQAMEAQLT	Oy 341 SAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIEQFNVNNP 392	QY 285 LIDAAETKVNE-LKQEHTGLTDSPLVKKAEEQISQAQKDIQEIKPSGSDIPIVGPSG 340 : : : : : : : : : : :	1660 SVSDSTSDSTSASTSGSMSVSISLSDSTSTSTSASEVMSASISDSQSMSESVNDSESVSE 594 SKAPQFGYFAVQNSADSLQKFAAQLEREFVDGERSLAES 632 1 : : : : : : : : : :	Db 1604 -STSASGSASTSTSTSDSRSTSASTSTSMRTSTSDSQSMSLSTSTSTSMSDSTSLSD 1659 Qy 560 VYSRLQVLDSLMSTIVSNPQANQEEIMOKLTASI 593
	Oy 116 SGLENAKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVN 158 : : : : :	Qy 62 AKNALISLRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAK 115 : : : : : : : : :	Qy 10 SGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSS 61 :	Query Match 7.3%; Score 235; DB 2; Length 2285; Best Local Similarity 19.3%; Pred. No. 0.034; Matches 159; Conservative 141; Mismatches 312; Indels 210; Gaps	Oy 548 ETYPROSOTLEDVISKLOV_LESLASTIVSMPONNOEELM	

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EATPEQILVNGELIVHRD 6155
                         EREFVDGERSLAESQENA 636
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                                                                                                                                       RSGIESQGRSADASQRAA 547
EVTLLDGSKVIVNVPVKV 6212
                                                                         ----EEIM----- 586
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D:g3025510; PIDN:AAC13005.1
A.M.; Alloni, G.; Azevedo, V.; Ber
L, B.; Capuano, V.; Carter, N.M.;
rington, J.; Fabret, C.; Ferrar1, ct, H.; Mauel, C.; Karamata, D. text_change 15-Oct-1999 he Bacillus subtilis SPbetac2 pro

jita, Y.; Fuma, S.; Galizzi, A.; Gal Holsappel, S.; Hosono, S.; Hullo, M. M.; Kurita, K.; Lapidus, A.; Lardino Levine, A.; Liu, H.; Masuda, S.; Mau S.H.; Parro, V.; Pohl, T.M.; Portete ose, M.; Sadaie, Y.; Sato, T.; Scanl F.; Sekiguchi, J.; Sekowska, A.; Se P.; Tognoni, A.; Tosato, V.; Uchiya K.; Yasumoto, K.; Yata, K.; Yoshida wa, H.; Danchin, A. on not shown

2; Indels 210; Gaps 4478; PIDN:CAB14053.1; PID:e11835 Length 2285; 33;

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A; Experimental : C; Genetics: A; Gene: yihD
                                                                                                                                                                          C; Accession: D86731 A.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus A; Reference number: A86625; MUID:21235186; PMID:11337471

A; Accession: D86731

A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1063 <STO>
A; Cross-references: GB:AE005176; PID:g12723779; PIDN:AAK04950.1; GSPDB:GN00146
A; Experimental source: strain IIL1403
                             멍
                                                                                                                                                                                                                                                                                                                                         hypothetical protein yihD [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis C;Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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----SAKNALISLRDAILNKNSSPTDSLSQ-----LEASTSTSTVTRVAAKD-YDEAK 108
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                                                                                       Conservative 108;
                                                                                     7.3%; Score 234; DB 2; J
22.4%; Pred. No. 0.013;
Live 108; Mismatches 285;
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A;Gene: lm
A;Genetic
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A;Title: Selection of Mycoplasma hominis PG21 deletion mutants
A;Reference number: Z18884; MUID:95369882; PMID:7543881
A;Accession: T30822
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Impl protein - Mycoplasma hominis
C:Species: Mycoplasma hominis
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
C:Accession: T30822
                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U21962; C;Genetics:
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-1365 <JEN>
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Best Local Similarity
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LRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAK-DYDE-----AKSNFDTAKSGLENA 121
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                                                                                                                                             149;
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                                                                                                                                           Conservative 137;
                                                                                                                                                              7.2%; Score 231;
21.5%; Pred. No. 0.
                                                                                                                                                                                                                                                                                     NID:g790243; PID:g790244; PIDN:AAA81013.1
                                                                                                                                             Mismatches
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probable myosin heavy chain [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84730
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A.;Accession: F84730
A.;Status: preliminary
A,;Molecule type: DNA
A;Residues: 1-1269 <STO>
A;Cross-references: GB:AE002093; NID:g6598483; PIDN:AAC69932.2; GSPDB:GN00139
C:Genetics:
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A; Map position: 2
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    62
                                                                                                                                                 Local Similarity
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                                              LKSTKESAKEMEEKMASLQQEIKELNEKMSENEKVEAALKSSAGELAAVQEE-----LAL
  AKNAL-----ISLRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAKSNFDTAK 115
                                                                                   MESGPESVSSNQSSMNPI-----INGQIASNSETKESTKASEASPSASSSVSSWSFLSS
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                                                                                                                               Conservative
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                                                                                                                           7.1%; Score 226.5; DB 20.8%; Pred. No. 0.035; tive 142; Mismatches 28
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                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                               surface-located membrane protein lmp3 precursor - Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C;Accession: JC6009

R;Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G. J. Bacteriol. 178, 2775-2784, 1996
A;Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp A;Reference number: JC6009; MUID:96213016; PMID:8631664
A;Accession: JC6009; MUID:96213016; PMID:8631664
                                                                                                                                                                                    C;Genetics:
A;Gene; Imp3
A;Genetic code: SGC3
A;Genetic code: SGC3
C;Superfamily: surface-located membrane protein lmp3; t
C;Keywords: duplication; membrane protein protein c;Keywords: duplication; membrane protein for c;Keywords: duplication; membrane protein lmp3; t
                                                                               F;25-1302/Product: surface-located membrane protein Lmp3 *status F;957-992/Domain: tetratricopeptide repeat homology <TT1>F;957-992/Domain: tetratricopeptide repeat homology <TT2>F;1089-1120/Domain: tetratricopeptide repeat homology <TT3>F;1154-1190/Domain: tetratricopeptide repeat homology <TT4>
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A; Residues: 1-1302 < LAD>
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    150;
                          Similarity
    Conservative
                                                                                                                                                                                                                                                                                                                          EMBL: X95601; NID: g1197335;
                        21.6%;
                                            7.0%;
    139;
                        Score 225.5; D
Pred. No. 0.04;
      Mismatches
                                                                                                                                                                                                                                                                                                                          PIDN:CAA64858.1;
                                            DB 1;
    223;
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      Indels
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Transport protein USO1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D2552; protein YDLO58w
C;Species: Saccharomyces cerevisiae
C;Bate: 12-Jul-1996 **sequence_revision 12-Jul-1996 **text_change 21-Jul-2000
C;Accession: S67593; A38455; S30782
R;Bloecker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67587
A;Accession: S67593
A;Molecule type: DNA
A;Residues: 1-1790 <BLO>
A;Cross-references: EMBL:Z74106; NID:g1431058; PID:e253003; PID:g1431059; MII
A;Title: A cytoskeleton-related gene, USO1, is required for intracellular prof; Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.
Cell Biol. 113, 245-260, 1991
A;Title: A cytoskeleton-related gene, USO1, is required for intracellular prof; Reference number: A38455; MUID:91185402; PMID:2010462
A;Recession: A38455
A;Molecule type: DNA
A;Residues: 1-389, 'TA', 392-724, 'S', 726-1790 <NAK>
A;Cross-references: GB:X54378; NID:g4777; PIDN:CAA38253.1; PID:g4778
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F; 326-342/Domain: transmembrane *status F; 394-410/Domain: transmembrane *status F; 617-633/Domain: transmembrane *status
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A;Description: An integrin analogue in Saccharomyces cerevisiae.
A;Reference number: S30782
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A; Residues: 71-846,'E',848-923,'K',925-1252,'I',1254-1318,'V',1320-1460,'S',1462-1580
A; Cross-references: EMBL:L03188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: coiled coil; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
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SKLEDIERELKDKQAEIKSNQE
                                                                        DLISRINESEKDIEELKSKLRIEAKSGSELETVKQELNNAQEK---IRINAEENTV--LK
                                   KFAAQLEREFVDGERSLAESQE
                                                                                                         DVYSRL----QVLDSLMS--TIVSNPQANQEEIMQKLTASISKAPQFGYPAVQNSADSLQ
                                                                                                                                                KLESTIESNETELKS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLEK-----EHEDLAAQLKKYEEQIANKERQYNEEISQLNDEITSTQQENESIKK-- 1198
                                                                                                                                                                                      TLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQRAAETIVRDSQ-TLG
                                                                                                                                                                                                                                                                                                 NDELLEEKQNTIKSLQDEILSYKDKITRNDEKLLSIERDNKRDLESLKEQLRAAQE----
                                                                                                                                                                                                                                                                                                                                                                            --KERKLLNEGSST---ITQEYSEKINTLEDELIRLQNENELKAKEIDNTRSELEKVSLS
                                                                                                                                                                                                                                                                                                                                                                                                             VGPSGSAASAGSAAGALKSSNNSGRISLLLDDV-----DNEMAAIALQGFRSMIEQFNVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DMERLANSDPSNNHTEEVNNIKKALE--AQK-----DTIDKLN-KLVTLQNQNKSLTEVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AELAAYKNLKNELETKLETSEKALKEVKENEEHLKEEKIQLEKEATETKQQLNSLRANLE 1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TKESTKASEASPSASSSVSSWSFLSSAKNAL---ISLRDAILNKNSSPTDSLSQLE
                                                                                                                                                                                                                                                            DGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAAET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TDSPLVKKAEEQISQAQKDIQEIKPSGSDIPI
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                                                                                                                                                -SMETIRKSDEKLEQSKKSAEEDIKNLQHEKS 1554
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02-Sep-2000

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myosin heavy chain - Entamoeba histolytica
C:Species: Entamoeba histolytica
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C:Accession: T18296
R:Guillen, N.
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A;Residues: 1-2139 <GUI>
A;Cross-references: EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AAB48065.1
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                                                                                                                  NKNSADQIIKDL------ERQNISYEAVLTNAGEVIKASSEAGIKLGQALQSIVDAG
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                     VQNNQLQATNKELKAKDNDLTSKIE----
                                                      IVSNP-QANQEEIMQK----LTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSL
                                                                                                                                                                                                                                            KEKQVKKLEGELKETKDKLNAAI-AEKDSIFTAKKQSDAD-
                                                                                                                                                                                                                                                                                                                        QRDKLVADNKKMTKTLEEIKARDEENTYKVENYEKVLKRKEADLEEANENLDIEKKDRMN 1453
                                                                                                                                                                                                                                                                                                                                                         GRISLLLD-------DVDN----EMAAIALQGFRSMIEQFNVNNPATAKELQA 400
                                                                                                                                                                                                                                                                                                                                                                                                ESKNKDSENEKAALSEEIDQANEKLKNIQ---ADL----RKATADLQEANEKKAEVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEKLKAKAKDLEAQLNEVQDNHEKAVADAELLNKKKAQSDKELNSLKAELEALTKAKSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQ---SQAAVLQAQQNNSPDN---IAATKELID----AAETKVNELKQEHTGLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKEDAEKKKKEIEKEMKALQEEKENVESS - - - KNSTEKDKKKLEDNLKDTQKKLDDMTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGADVSQYLQKQKEEYESQIAKMQEEKEAIGNDVKNKEKTIKEKELEIQSLQEKLDETEV
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                                                                                             SELEEQVNELESRPYGTG----
                                                                                                                                                                                                     AGTAGTVQMNVKQLYKTA----FSSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVQ--
                                                                                                                                                                                                                                                                               MEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMGQVAFAAAKVGGGS
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20.9%; Pred. No. 0.14;
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                                                                                             --NADEN---
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                   -ITENEMKKLENAKKRLEQDKDEADKAV 1637
                                                                                           -EIKIRDAQ-IADLNKALE-----MKG
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A; Molecule type: CANDIS
A; Residues: 1-2570 <MUHS
A; Cross-references: EMBL:AF100426; NID:g3929311; PID:g3929312; PIDN:AAC79868.1
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R:Wu, H: Fives-Taylor, P.
Submitted to the EMBL Data Library,
Nucleotide sequences
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C;Date: 02-Sep-2000 #sequence_revision
C;Accession: T17451
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                                    SESISESVSESVSESISESVSESVSESISESVSESISE-SVSESVSESIXESVSES
                                                                       SRSVSRSGIE--SQGRSADASQRAAETIVRD-SQTLGDVYSRLQVLDSLMSTIV-SNPQA
                                                                                                            TVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRS-GVQSAISQTANPAL
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288; 2;

Indels Length

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343 350 294 297

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On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; HOILZAPP ISON, T.; Hickey, E.K.; Helt, I.E. Science 293, 498-506, 2001

A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Reference number: A95000; MUID:21357209; PMID:11463916

A; Status: preliminary

N. M. Status: preliminary
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A;Residues: 1-4776 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75846.1;
A;Experimental source: strain TIGR4
C;GenetLcs:
A;Gene: SP1772
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                                                                                                                                                SSSYAAALSDGYSAYKTLNSLYSESRSGVQSA---ISQTANPALSRSVSRSGIESQGRSA
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Radune, D.; Holtzapple,
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A; Residues: 1-2055 <MAN>
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                                     AKKAAI--TANNALTQEEKAAAIKQVEDEAAKAQAAVDASRSKADVDRAKDQGLQKISDV 1170
                                                                        GVQSAISQTANPALSRSVSRSGI---ESQGRSA----DASQRAAET-IVRDS--QTLGDV 560
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                                                                                                                                              --AKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGY-SAYKTLNSLYSESRS
                                                                                                                                                                                                                                                                TQKAQATAATEAAEQAKRLELQGRNDLTTEERNNALADLTAKAQAAKDAVNQARNNTGVA
                                                                                                                                                                                                                                                                                                     ---AKELQAMEAQLTAMSDQLVG------ADGELPAEIQAIKDALAQALKQPSAD 440
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                                                                                                           RDAKAAIDRAGSNGDVNNAVNQ-GKAAIQAIK-----ALDDSQPSAKDTAKAAIQNAAD
                                                                                                                                                                                      GAKDNGVAQIQGINPTAVVKPDARNAIDQAARDKEAEFQANTKLTDEEKAAAIKKVQDAA 1059
-YSRLQVLDSLMS---TIVSN----PQANQEEIMQKL---
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Pred. No. 0.18;
24; Mismatches 27
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extracellular matrix binding protein - Abiotrophia defectiva (fragment) C;Species: Abiotrophia defectiva C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C;Accession: T31110 R;Manganelli, R.; van de Rijn, I. Infect. Immun. 67, 50-56, 1999 A;Title: Cloning and characterization of emb, a gene encoding the major adhe A;Reference number: Z20988; MUID:99081722; PMID:9864195 A;Accession: T31110 A;Cross-references: EMBL:AF067776; NID:g3249002; PID:g3249003; 2; Length PIDN: AAD03320.1 major adhesin of

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501 GPETL------PVVAALRIVPRYNSGQVVPEHRMTSGNATNAAPTIAVTTPSTTLNVD 552 11 GPESVSSNQSSMNPII------NGQI-----ASNSETKESTKASEASPSASSSVS SWSFLSSAKN--ALISLRDAILNKNSSPT------DSLSQLEASTSTSTVTRVAA 101 272; Indels 263; Gaps 54 42;

IKKA-LEAQKDT----IDKLNKLVTLQN--QNKSLTEVLKTTDSADQIPAINSQLEINKN 212 KDYDEAKSNEDTAKSGLENAKTLAEYETKMADLMAALQDMERLANS--DPSNNHTEEVNN QAISDATIKSMVRVNDLEDDARQTNGTPVQADIVSYSKNGQTVAAIDPTVEGEYTVTLRA AVNKINEISQRPDLTREEKQAFMDQVRTARDAAMAKVASAANNQAVTSARDQGLNAV---AEKAKVEAAKNATLAGIDQA-KTTAARNAAQNKGTTDINAVNPVPVAKPAANAALE--QA -- NNLPTPAAKYPEALGHVRQAADAKRQAIRDNANLTAEEQADALRQVDAAQTAAEAAIN SADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIKLGQAL--QSIVDAGDQSQAAVLQA 270 RDSQDKLSN-NTVQ--VKVAFTLPREEAK-----NAVNNAAKAKNTAIDNNNNLTAEEKA -DNIAATKE------LIDAAETKVN-ELK 836 721 612 357 297 159 778

----ATAMGOVAFAA 453

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A; Experimental source: strain C; Genetics: A; Gene: yqfG
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A;Title: The complete genome sequence of the lactic acid bacterium A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86827
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                                                                SSSENSAASILTSYSNNNSESSETGCLYISNEAQRDNGSEISHSLPSSNSNENNVSSIQS
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C;)ate: 10-May-2001 #Sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: H89960 #Sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: H89960 #Sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: H8960 #Sequence_revision 10-May-2001 #text_change 22-Oct-2001 C; Shiba, T; Kohayashi, N; Baba, T; Yuzawa, H; Kohayashi, I; Cui, L; Rma, A; Miautani-Ui, Y; Kohayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K. Lancet 357, 1225-1240, 2001 #Sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146 A; Accession: H89960
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A;Residues: 1-2186 <KUR>
A;Cross-references: GB:BA000018; PID:913701552; PIDN:BAB42845.1; GSPDB:GN00149
A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SA1577 [imported] - Staphylococcus aureus (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                               DLERQNISYEAVLTNA----GEVIKASSEAGIK--LGQALQSIVDAGDQSQAAVLQAQQN
                                                                                                                                                                                                                                                                                                                                                                                                                              DERDVAIDTLNKIVNTIKNDIAQNKTNAEVDRTETDGNDNIKVILPKVQ-----VK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDAAVTDVRNQTIKAIEQIKPKVRRKRAALDSIE-----ENNKNQLDAIRNTLDTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDTAKSGLEN--AKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIK----ATAENQVESIKD-----TPHATVDELDEANQLISDTLKQAQQEIE--NTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVSSWSFLSSAKNALISLRDAILNKNSSPTDSLSQL-EASTSTSTVTRVAAKDYDEAKSN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERS-----LAESQENAFRKQPAFIQ
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    DGELPAEIQAIKDALAQALKQPSA-----DGLA--TAMGQVAFAAA----KVGGGSAGTAG
                                                     INRKASAREQLTTLFNDKKQAIEANIQATVEERNSILAQLQNIYDTAIGQIDQDRSNAQV
                                                                                                                                                                                                                                       IDAQNIISKIKPATTVKATALQQIQNIATNKINLIKANNEA-TD-----EEQNIAIAQ
                                                                                                 LQGFRSMIEQ----FN------VNNPATAKELQAMEAQLTAMSDQLVG-----------A
                                                                                                                                                                                           AQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAI--A
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21.3%; Pred. No. 0.
                                                                                                                                                                                                                                                                       AATKELIDAAETKVNELKQEHTGLTDSPLVKKAEEQ---ISQ 318
                                                                                                                                                  ----IASAVTNADVAYLLHDEKNEIREIEPV
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QY 372 MAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAI 426 :	QY 22 ALQSIVDAGQQQAAVLQAQQNASDNIAATKELIDAAETKVNELKQEHTGLTDSPLVKK 311	151NNHTEEVNNIKKALEAQKDTIDKLNKLUTLQNQNKSLTEVL	Qy 56WSFLSSAKNALISLRDAILNKNSSPTDSLSQLEASTSTYTTRVAA 101 Db 989	Ouery Match 6.6%; Score 212; DB 2; Length 1690; Best Local Similarity 19.3%; Pred. No. 0.21; Matches 136; Conservative 133; Mismatches 300; Indels 134; Gaps 26; Qy 4 HHHHMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSS-55 1 : : : :	RESULT 19 T13030 microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Cate: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C;Accession: T13030 R;Lantz, V.A.; Miller, K.G. J. Cell Biol. 140, 897-910, 1998 A;Title: A class VI unconventional myosin is associated with a homologue of a microtubu: A;Reference number: Z17588; MUID:98139549; PMID:9472041 A;Accession: T13030 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1690 <lann a;cross-references:="" a;experimental="" c;genetics:="" c;keywords:="" cytoskeleton<="" embl:af041382;="" flybase:fbgn0020503="" nid:92773362;="" oregon="" pid:92773363;="" pidn:aab96783.1="" r="" source:="" strain="" th=""><th>Db 1947 DKTASLNLQTIHDLDVHPIKKPDAEKTINDDLARVTALVQNYRKVSNRNKADALKAITAL 2006 Qy 466 TVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVOSAISQTAN 521 LII: </th></lann>	Db 1947 DKTASLNLQTIHDLDVHPIKKPDAEKTINDDLARVTALVQNYRKVSNRNKADALKAITAL 2006 Qy 466 TVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSESRSGVOSAISQTAN 521 LII:
OY 383 MIEQFIVVNNPATAKELQAMEAQLTGAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGL 442	Qy 291	203 INSQLEI :: 1134 IAAKL 259 AG 259 KGKAELE	Qy 118 LENAKTLAEYETKMADLMAALQDME-RLANSDPSNNHTEEVNNIKKAL- 164 ;	OY 15 VSSNQSSMNPIINGQIASNSETKESTKAS-EASPSASSSVSSWSFLSSAKNALISLRDAI 73 :: :	RESULT 20 S33441 EF protein - Streptococcus suis C:Species: Streptococcus suis C:Species: Streptococcus suis C:Species: Streptococcus suis C:Cacesion: S34441 R:Smith, H.E.; Reek, F.H.; Vecht, U.; Gielkens, A.L.J.; Smits, M.A. Submitted to the EMBL Data Library, May 1993 A;Description: Repeats in an extracellular protein of wek-pathogenic strains are abse A;Reference number: S33441 A;Accession: S33441 A;Status: preliminary A;Molecule type: DNA A;Residues; 1-1822 <smi>A;Residues; 1-1822 <smi>A;Residues; 1-1822 <smi>A;Cross-references: EMBL:X71880; NID:g298031; PIDN:CAA50714.1; PID:g298032 Ouery Match Best Local Similarity 19.6%; Score 211.5; DB 2; Length 1822; Matches 147; Conservative 131; Mismatches 300; Indels 171; Gaps 30;</smi></smi></smi>	Db 1384 KEALCQKENGLKELQGKL

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A;Status; preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: I-2481 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701961; PIDN:BAB43253.1; GSPDB:GN00149
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: D90011
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D90011
D: VICOLS UP COLUMN C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDVITPTVKPQAKQDIIQAVTTRKQQIKKSNASLQDEKDVANDKIGKIETKAIKDIDAAT 718
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KQAIADKVQAQETAIDANNGSTTEEKEAAKQQ----VQTEKTAADAAIDAAHSNVEVEAAK 1112
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                                                                                                                                                                             SQAQKDIQEIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIA 376
                                                                                                                                                                                                                                                                                                                                                                                                                        AIQTQAKVKPAADTEVENAYNTRKQEIQNSNASTTEEKEAAYTELDAKKQEARTNLDAAN
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                                                                 LQGFRSMIE----QFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPA-----EIQAIK 427
                                                                                                                                                                                                                                                                               TNSDVTTAKDNGIAAINQVQAATTKKSDAKAEIAQKASERKTAIEAMNDS----TTEEQQ 1005
                                                                                                                                                                                                                                                                                                                                            NNS------GLTDSPLVKKAEEQI 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ISYEAVLTNAGEV-----IKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQ
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                                                                                                                                         -DNATANTDVDNAKTTNEA-TIAAITPDANVKPA--A
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Pred. No. 0.41;
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hypothetical protein C18C4.5 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change C:Accession: T34107 R:Gattung, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1091 <GAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, April A; Description: The sequence of C. elegans A; Reference number: Z21478
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Best Local Similarity
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                                   QSIVDAGDQSQAAVLQAQQNNSPDNI--AATKELIDAAETKVNELKQEHTGLTDSPLVKK 311
                                                                                                                                                                                                                                                                                                                                        SAKNALI-SLRDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDVDEAKSNFDTAKSGLE 119
                                                                                                                                                                                                                                                                                                                                                                                      MEQEIENLQRQLNIKTASLQSLMLAKSDSSKTDKLSEENETLKLKVEDLQKQVSSFMSQM 167
                                                                                                                                                                                                                                                                                                                                                                                                                            MESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPS-----ASSSVSSWSFLS
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RQLQKMSEQRQNEEVARQGEDSARSMEEKATKEEIKKLKSQV-QLQQQLE--QDLELQKK
                                                                           TEEKYQ-----QAQKKIENLDETIKQQETQ-----
                                                                                                             TDSADQIPAINSQLEINKNSADQIIKDLERQNISYEAVLTNAGEVIKASSEAGIKLGQAL 253
                                                                                                                                                                                                                                 TSESTLSMLKDKLAQFEQNALDLKNENAQMKTSTRESILFESGRIKELQQALSDEKDNNA
                                                                                                                                                                                                                                                                       NAKT-----LAEYETKMADL-----
                                                                                                                                                                                                                                                                                                             QDKNSETQKMKDAISVNDVSRQNMDSLSEKLSEMDRTLREEQQQKSQLRSQTETLKNALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQLQ---ATQTNVINNDQNATNEEKEAAIQQLATAVTDAKNNITAATDDNGVDTAKDAGK 1347
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                                                                                                                                                     ILNVQLREKDGKIDRIQVDLLAAESRAQQAEEDVRDMKERIITSKKDDDSNNLLQDELRR
                                                                                                                                                                                           -----HTEEVNNIK------KALEAQKDTIDKLNKLVTLQ---NQNKSLTEVLKT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136;
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38/3; 95/3; 179/2; 259/3; 301/3; 419/2; 573/3; 613/1;
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Db 124 STNAQLSSSTTETDSISSSAIQTSSPQTSSSNGGGSSSEPLGKSSVLETTAS 175 Qy 116 SGLENAKTLAEYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLN 175	Query Match G.5%; Score 208.5; DB 2; Length 1104; Best Local Similarity 19.6%; Pred. No. 0.17; Matches 122; Conservative 109; Mismatches 271; Indels 121; Gaps 17; Matches 122; Conservative 109; Mismatches 271; Indels 121; Gaps 17; Qy 12 PESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLS 60	C;Species: Saccharomyces cerevisiae C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002 C;Accession: S59310 R;Churcher, C.M. Submitted to the EMBL Data Library, September 1995 A;Reference number: S59302 A;Accession: S59310 A;Molecule type: DNA A;Residues: 1-1104 <chu> A;Cross-references: EMBL:Z54141; GSPDB:GN00013; MIPS:YMR317w A;Cross-references: EMBL:Z54141; GSPDB:GN00013; MIPS:YMR317w A;Cross-references: STRAIL: STRAIN AB972 C;Genetics: MIPS:YMR317w A;Cross-references: SGD:S0004936 A;Map position: 13R</chu>	Oy 582 QEEIMQKLTASISKAPQFGYPAVQNSADSLQKFAAQLEREFVDGERSLAESQEN 635 :	Qy 465 GTVOMNVKOLYKTAFSSTSSSYAAALSDGYSAYKTLNSLYSESRSGVQSAISQTANP 522	Qy 312 AEBQISQAQKDIQEIKPSGSDIPIVGPSGSAASAGSALKSSNNSGR 360 Color
: : : : : :		A; Reference number: Z19645 A; Accession: T22976 A; Accession: T22976 A; Accession: T22976 A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1133 <wil> A; Cross-references: EMBL:Z34801; PIDN:CAA84332 A; Experimental source: Clone F59A2 R; Burton, J. submitted to the EMBL Data Library, October 19 A; Reference number: Z19700 A; Reference number: Z19700 A; Accession: T23157 A; Status: preliminary; translated from GB/EMBL A; Molecule type: DNA A; Residues: 1-1133 <wiz> A; Cross-references: EMBL:Z66514; PIDN:CAA91344 A; Experimental source: Clone KO1A11</wiz></wil>	al protein F59A2.6 - Caeno Caenorhabditis elegans (-Oct-1999 #sequence_revis n: T23976; T23157	Qy 512 VQSAISQTANPALSRSVSRSGIESQGRSADASQRAA : : : : : :	Qy 345 AGSAAGALKSSNNSGRISLLLDDVDNENAAIALQGF

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SFRSMIEQENVNNPATAKELQAMEAQ 404
| | : | : | | | | | |
SLASS-RLFSSKNTSVTSTLVATEAS 438
AETIVRDSQTLGDVYSRLQVLDSLM 571
                                                                                       ETLASNSIIESSLSTGYNSTVSTTT 473
                                                                                                        DGLAT-----AMGQVAFAAAKV 456
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3L/DDBJ 2.1; GSPDB:GN00021; CESP:F59A2.6 -1999 #text_change 29-Oct-1999

3L/DDBJ 1995

4.1; GSPDB:GN00021; CESP:F59A2.6

DB 2; Length 1133;).18; nes 279; Indels 163; 67/3; 635/3; 710/3; 738/3; 795/2; 1008/3 Gaps 25;

XINSQLEINKNSADQIIKDLE--RQN 225 | | |:| | : |: XITKQMEAAKKELEASEKEKSELREQ 318 SSVSS-----WSFLSSAKNALI 67 DQSQAAVLQAQQNNSPDNIAATKEL 285 KDYDEAKSNEDTAKSGLENAK---- 122 EKLNSEQNILDEVTKKLEQSEEEVL 147

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1306 <RIE>
A;Cross-references: EMBL:Z72799; NID:g1322977; PID:g1322978; MIPS:YGR014w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSB2 protein - yeast (Saccharomyces cerevisiae) R;Alternate names: protein G4017; protein YGR014w C:Species: Saccharomyces cerevisiae C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 C:Accession: S25370; S64305
                                                            밁
                                                                                                                                                                                                          C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; C;Keywords: transmembrane protein F;3-19/Domain: transmembrane #status predicted <TM1>F;1189-1205/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the Protein Sequence Database, A; Reference number: S64071
A; Accession: S64305
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S25370
MSB2 pi
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A; Residues: 1-1306 <BEN>
A; Cross-references: GB: M77354; NID: g171993; PIDN: AAA34798.1;
A; R; Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
R; Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: A Ser/Thr-rich multicopy suppressor of a cdc24 bud A; Reference number: S25370; MUID:92383951; PMID:1514328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bender, A.; Pringle, J.R.
Yeast 8, 315-323, 1992
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                                                                                                                                      Matches
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                                                                                                                                                    Local Similarity
                   VSSWSFLSSAKNALISL----RDAILNKNSSPTDSLSQLEASTSTSTVTRVAAKDYDEAK 108
                                                                                               SGPESVSSNQSSMNPIINGQIASNSETKEST----
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                                                        NGTQQAQSQSES-----QGQVSFTNEASQDSSTTSLVTAYSQGVHSHQSATIVSATISSL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEKEEKLEMVKVQLQQAAQSSSSVEQALRAEIEKLEAKLQEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSA-----YKTLN
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                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                        SGD:S0003246; MIPS:YGR014w
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                                                                                                                                    100;
                                                                                                                                                      Score 208; DB Pred. No. 0.22;
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                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              May 1996
                                                                                                                                                                     DB 2;
                                                                                                                                    258;
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                                                                                                                                                                     Length 1306;
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                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans co. A;Reference number: Z21321 A;Accession: T33318
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33318
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                                                                                                                                                                                                          A; Gene: CESP: ZK1055.1
A; Map position: 5
                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1475 <GEI>
                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                  Query Match
Best Local :
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Geisel, C.; Bradshaw,
                                                                                                                   Matches
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                                                                                                                                  Local Similarity
                                                                          HMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNAL
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 ISLRDAILNKNSSPTDSLSQLEASTSTSTV----TRVAAKDYDEAKSNFDTAKSGLENAK 122
                                       HLTSSNEKIAELTSSLEMVAAQLLSSQQETDVAVTKVENLELKMEEAHRMYLLD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSTWYDASSTSQTSVSYASQESDYAVNQNSW-SASTNQLPSTSTTSYYAPTFSTSADFAA
                                                                                                                   Conservative 133;
                                                                                                                                                                                         218/2;
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                                                                                                                                                                                         385/3; 486/3; 1124/3; 1212/3; 1400/2
                                                                                                                                  6.5%; Score 208; DB 2; 18.2%; Pred. No. 0.26;
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                                                                                                                                                  Length 1475;
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                                                                                                                   208;
                                                                                                               Gaps
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A; Experimental s
C; Genetics:
A; Gene: ebhB
                                                                                             A;Molecule type: DNA
A;Residues: 1-3890 <KUR>
A;Cross references: GB:BA000018; PID:g13701233; PIDN:BAB42528.1;
A;Experimental source: strain N315
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                                                            QGAINDEQ-----TTLNSQNYQDATPSKKTAYTNAVQAAKDILNKSNGQNKTKDQVTEAM
                                                                                        QA--NQEEIMQKLTASISKAPQFGYP-----AVQNSADSLQKFAAQLE------
                                                                                                                        GDEKLVQSKTDAARAIDALPHLNNAQKADVKSKINAASNIAGVNTVKQQGTDLNTAMGNL
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                              -----REFVDGERSLAESQENAFRKQPAFIQQVLVNIASL
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A;Title: DNA Sequence of bo A;Reference number: A82035; A;Accession: C82206 methyl-accepting chemotaxis protein VC1403 [imported] - Vibrio cholerae (strain C;Species: Vibrio cholerae C;Decies: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: C82206 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000 A; Molecule type: DNA A; Residues: 1-641 <H A; Status: preliminary

both chromosomes of the cholera pathogen 35; MUID:20406833; PMID:10952301

Vibrio

cholerae

Gwinn, M.L.; Dodson, R.
H.; Dragoi, I.; Sellers

N1696

RESULT

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A;Cross-referen
A;Experimental
C;Genetics:
A;Gene: VC1403
A;Map position:
                                                         myosin heavy chain-B, neuronal - chicken N:Contains: myosin ATPase (EC 3.6.4.1) C:Species: Gallus gallus (chicken) C:pate: 31-Dec-1993 #sequence_revision 31-Dec-1993 C:Accession: B43402; A43402 R;Takahashi, M: Kawamoto, S: Adelstein, R.S. J. Biol. Chem. 267, 17864-17871, 1992 A:Title: Evidence for inserted sequences in the hea
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                                                                                                                                                                                                                                                           QSSSTSELASAIENIAAVADELQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKD-----ISNGAEMVSNG--VKSSSQKAESEVQKGHVVNKQLTLIRNEMVDLVKDSEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148;
type: mRNA
                B43402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                  MUID:92388144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 207.5; DB 2;
Pred. No. 0.088;
5; Mismatches 252;
                                                                                                                                                                                                                                                           640
                                                                                                                                                                                                                                                                                        572
                                  PMID:1355479
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                                                             head region
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El Tor
                                                              of nonmuscle myosin specifi
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A;Molecule type: mRNA
A;Residues: 1-211;222-631;653-2007 <TA2>
A;Residues: 1-211;222-631;653-2007 <TA2>
A;Residues: 1-211;222-631;653-2007 <TA2>
A;Residues: 1-211;222-631;653-2007 <TA2>
A;Rote: sequence extracted from NCBI backbone (NCBIN:112864)
C;Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmusc C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Reywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; metl
F;1-2007/Product: myosin heavy chain-B, neuronal #status predicted <MYN>
F;1-211,222-631,653-2007/Product: myosin heavy chain-B, nonmuscle #status predicte
F;88-802/Domain: myosin motor domain homology <MMOTP>
F;18-185/Region: alternatively spliced segment 1 #status experimental
F;559-593/Region: alternatively spliced segment 2 *status experimental
F;632-652/Region: actin binding #status predicted
F;632-11/4/Region: actin binding #status predicted
F;632-61/4 (Region: actin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:875-2007/Domain: coiled coil *status predicted <COI>F:875-1315/Region: S2
F:875-1316-2007/Region: light meromyosin
F:129/Modified site: N6.N6-trimethyllysine (Lys) *status
F:184/Binding site: ATP (Lys) *status predicted
F:732.742/Active site: Cys *status predicted
F:732.742/Active site: phosphate (Thr) (covalent) *status pred
F:1987/Binding site: phosphate (Ser) (covalent) *status pred
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AALSDGYSAYKTLNSLYSESR---
                                            ALAVAAKKKMEMDLKDLEGQI - - EAANKARDEA - -
                                                                                       ALAQALKQPSADGLATAMGQVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYA
                                                                                                                                      LRLEVNMQAMKAQFE - -
                                                                                                                                                                                 ----IALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKD--
                                                                                                                                                                                                                                DLMSSKDDV---
                                                                                                                                                                                                                                                                          EIKPSGSDIPIVGPSGSAASAGSAAGALKSSNNS-----GRISLLLDDVDNEMAA-----
                                                                                                                                                                                                                                                                                                                       LAEEKNISARYAEERDRAEAEARE--KETKALSLARALEEALEAKEEFERQNKQLRADME
                                                                                                                                                                                                                                                                                                                                                               IAATKELI------DAAETKVNELKQEHTGLTDSPLVKKA-----EEQISQAQKDIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGQALQSI---
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Pred. No. 0.
                                                                                                                                      RDLQARDEQNEEKKRMLVKQVRELEAELEDERKQR
·SGVQSAISQTANP-ALSRSVSRSGIESQGRSAD
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Db 421 KLETFNKDKEAFNELKOTRNQIQEFINTNKNNPNYSELISQLTSKRDSKNSVTDSS 477 Qy 341 SAASAGAALKSSNNSGTSLLLDDVDNEMAAIALQGFRSMIEQFNVNNPATAK 396	OY 165 EAQKDTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSADQIIKDLERQ 224 ::: :: : : : :	Qy 5 HHHMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSS 55 1	95369882; PMID:7543881 I from GB/EMBL/DDBJ NID:g790241; PID:g790242; PIDN:AAA81012.1 Score 204; DB 2; Length 1051; Pred. No. 0.24; Pred. No. 0.24; 2; Mismatches 315; Indels 122; Gaps 30;	SULT 30 8351 pl protein - Mycoplasma ho Species: Mycoplasma homini Date: 15-Oct-1999 #sequenc Accession: T18351 Jensen, L.T.; Ladefoged, S fect. Immun. 63, 3336-3347 Title: Selection of Mycopl	Db 1690 RELEEARASRDEIFAQSKESEKKLKGLEAEILQLQEEFAASERARHAEQERDELAD 1746 Oy 542 ASQRAAETIVRDSQTLGDVYSRLQVLDSLMSTIVSNPQANQEEIMQKLTASISKAPQ 598
A;Gene: unc-54; CESP:F1IC3.3 A;Gene: unc-54; CESP:F1IC3.3 A;Gene: unc-54; CESP:F1IC3.3 A;Introns: 21/3; 64/3; 111/3; 264/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3 A;Introns: 21/3; 64/3; 111/3; 264/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3 C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle C;Reywords: myosin motor domain homology <mmot> F:174-181/Region: nucleotide-binding motif A (P-loop) F:662-684/Region: actin binding #status predicted F:662-684/Region: actin binding #status predicted F:848-1963/Domain: coiled coil #status predicted <coi> F:848-1963/Region: S2 F:1163-1963/Region: light meromyosin</coi></mmot>	A; Molecule type: DNA A; Residues: 847-1333, 'R',1335-1876, 'L',1878-1963 <mcl> A; Residues: 847-1333, 'R',1335-1876, 'L',1878-1963 <mcl> R; Wills, N.; Gesteland, R.F.; Karn, J.; Barnett, L.; Bolten, S.; Waterston, R.H. Cell 33, 575-583, 1983 A; Title: The genes sup-7 X and sup-5 III of Caenorhabditis elegans suppress amber non A; Reference number: A21074; MUID:83232892; PMID:6571695 A; Accession: A21074 A; Molecule type: DNA A; Residues: 1873-1963 <mi3> A; Cross-references: GB:V01494; GB:J01049; NID:g6783; PIDN:CAA24738.1; PID:g6784</mi3></mcl></mcl>	le: eren essi ecul idue idue ss-r achl achl ec 29 e 29 e 29 e 29 essi	A; Accession: T20770 A; Status: translated from GB/EMBL/DDBJ A; Status: translated from GB/EMBL/DDBJ A; Status: translated from GB/EMBL/DDBJ A; Residues: 1-1963 <wil> A; Experimental source: clone F11C3 A; Experimental source: clone F11C3 A; Accession: T21629 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-1963 <wii2> A; Cross-references: EMBL:Z83107; PIDN:CAB05505.1; GSPDB:GN00019; CESP:F11C3.3 A; Experimental source: clone F32A7 B; Karn, J; Brenner, S.; Barnett, L. Proc. Natl. Acad. Sci. U.S.A. 80. 4253-4257. 1983</wii2></wil>	RESULT 31 MMKW myosin heavy chain B [similarity] - Caenorhabditis elegans N;Contains: myosin ATPase (EC 3.6.4.1) C;Species: Caenorhabditis elegans C;Date: 13-Unn-1983 #sequence_revision 19-May-2000 #text_change 19-Apr-2002 C;Accession: T20770; T21629; A93958; A93287; A21074; A02992 R;Kershaw, J. submitted to the EMBL Data Library, November 1996 A;Reference number: Z19322	Db 592 KNSNIGYRLFKLAQAEQFNNSDVDKLKNAWEEKQTLLSKKQKLGNQSTKDYLTQLSTEMS 651 Qy 497 AYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQRAA 547 :

2;

Length 1940

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R;Weston, D.S.; Schmitz, J.; Kemp, M.; Kunz, W.
Mol. Blochem. Parasitol. 58, 161-164, 1993
A;Title: Cloning and sequence characterization of a complete myos
A;Reference number: A59287; MUID:93211444; PMID:8459827
A;Accession: A59287
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1940 <WES>
A;Cross-references: GB:L01634; PIDN:AAA29905.1
A;Experimental source: strain Brazilian LE
C;Genetics:
A;Gene: MYH
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;82-752/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                       myosin heavy chain - fluke (Schistosoma mansoni) (strain c;Species: Schistosoma mansoni
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_C;Accession: A59287
R;Weston, D.S.; Schmitz, J.; Kemp, M.; Kunz, W.
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R;DeLozanne, i
Proc. Natl. A:
A;Reference n:
A;Accession: i
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N;Contains: myosin ATPase (EC 3.6.4.1)
C;Species: Dictyostelium discoideum
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 19-Apr-2002
C;Accession: A26655; A24728; S00250
R;Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986
           A; Molecule type: DNA
A; Residues: 1-2116 <ARAP>
A; Cross-references: GB:M14628; GB:M11938; NID:g167834;
A; Cross-references: GB:M14628; GB:M11938; NID:g167834;
R; DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.
Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985
A; Reference number: A24728; MUID:86016788; PMID:3901008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DS------LQKFAAQLERE----FVDGER-----SLAESQENAFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKGDLQRQLQKLQGELQQLRSRGGGGDVRSEEVEELKRKMNAKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQLSQLNKIKQQLSAQLEEARHSLEDE -- SRMKAKLNGEVRNLTSDLDS-LRETLEEEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAYKTLNSLYSESRSGVQSAISQTANPALSRSVSRSGIESQGRSADASQRAAETIVRDSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DQLDQANKAKAKAEKERSQFKAELDDAHNQV----DSIMKAKLNSEKTVKA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDLEAERAARSKAEKSR-----QQLESELEEVVDRL-EEQDGATAAQSDLTKKREAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEELKKDVEDLESSLQKAE--QEKQTKDNQIRTLQSEMAQQDEMIGKLNKDKKN--LEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDEAKSNFDTAKSGLENAKTLAEYETK-----MADLMAALQDMERLANSDPSNNHTEEV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SPTDSLSQLEASTS-----
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                                                                                     PIDN:AAA33227.1; PID:g167835
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A;Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostelium A;Reference number: S00250; MUID:88112226; PMID:2828113
A;Accession: S00250
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1734-1893 <WAG>
C;Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phosf;1-818/Domain: myosin motor domain homology <MAGT>
F;819-185/Region: nucleotide-binding motif A (P-loop)
F;819-2116/Domain: alpha-helical rod <ROD>
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A; Residues: 2035-2116 <DEL>
R; Wagle, G.; Noegel, A.; Sch
FEBS Lett. 227, 71-75, 1988
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Best Local Similarity
Matches 163; Conserv
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                                     LMSTIVSNPQANQEEIMQKLTASI--SKAPQFGYPAVQNSADSLQKFAAQLEREFVDGER
                                                                                                                                                KESELDEIKRQYADVVSSRDKS------VEQLKTLQAKNEELRNTAEEAEGQLDRAE
                                                                                                                                                                        ADGELPAEIQAIKDALAQALKQPSAD-------GLATAMGQV--AFAAAKVGGGSAGT
                                                                                                                                                                                                                                                                                                                                                                             KSTL-----EGEVARLQGELEAEQLAKSNVEKQKKKVELDLEDKSAQLAEETAAKQALDK 1227
                                                                                                                                                                                                                                                                                                                                                                                                                GSDIPIVGPSGSAA--SAGSAAGALKSSN---NSGRISLLLDD-----VDNEMAAIALQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEKKKKALDAMLEEMKDQLESTGGEKKSLYDLKVKQESDMEALRNQISELQSTIAKLEKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKETLKAMYDSKDALEAQKRELEIRVEDMESELDEKKLALENLQNQKRSVEEKVRDLEEE
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RLNEELSELRSVLEEADERCNSAIKAKKTAESALESLKDEIDAANNAKAKAERKSKELEV
                                                                                                           LSRSVSRSGIESQGRS------ADASQRAAETIVRDSQT-LGD---VYSRLQVLDS
                                                                                                                                                                                                                          ----LESELKHVNEQLEEEKKQKESNEKRKVDLEKEVSELKDQIEEEVASKKAVTEAKNK
                                                                                                                                                                                                                                                                                                   LKKKLEQELSEVQTQLSEANNKNVNSDSTNKHLETSFNNLKLELEAEQKAKQALEKKRLG
                                                                                                                                                                                                                                                                                                                                          FRSMIEQ-----
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                                                                          RSKKKAEFDLEEAVKNLEEETAKKVKAEKAMKKAETDYRSTKSELDDAKNVSSEQYVQIK 145.
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A:Molecule type: DNA
A;Residues: 1-971 <HAZ>
A;Cross-references: GB:BA000007; PIDN:BAB35073.1; PID:gl3361114; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable tail fiber protein [imported] -
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18
C:Accession: B9083
C:Accession: B9083
R:Hayashi, T.; Makino, K.; Ohnishi, M.; K
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DNA Res. 8, 11-22, 2001
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                                                                                             SSYAAALSDGYSAYKTLNSLY-SESRSGVQSAISQTANPALSRSVSRSGIESQGRSADAS
                                                                                                                              AGSATAAAQSKSTAESAATRAETAAKRAEDIASAVALEDASTTKKGIVQL-
                                                                                                                                                               IKDALAQALKQPSADGLATAMGQVAFAAAKVGGGSA-GTAGTVQMNVKQLYKTAFSSTSS
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N.; Yasunaga, T.; Kuhara, S.;
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Pred. No. 0.
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RESULT C85693

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probable membrane protein of prophage CP-933x Z1918 [imported] - Escherichia C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: C85693 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Eiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K Nature 409, 529-533, 2001
                                                                RESULT 36
S02771
supposin heavy chain A [similarity] - Cae
myosin heavy chain ATPase (EC 3.6.4.1)
N;Contains: myosin ATPase (EC 3.6.4.1)
C;Species: Caenorhabditis elegans
C;Date: 31-Dec-1993 #sequence_revision
C;Accession: T23622; S02771
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A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1918
                     submitted to
A; Reference
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A; Residues: 1-973 <STO>
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A;Accession: T23622
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-1992 <WILL>
A;Cross·references: EMBL:Z78199; PIDN:CAB01576.1; GSPDB:GN00023; CESP:K12F2.
A;Experimental source: Clone K12F2
R;Dibb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
J; Mol. Biol. 205, 603-613, 1989
A;Title: Sequence analysis of the complete Caenorhabditis elegans myosin healy reference number: S02771; MUID:89178677; PMID:2926820
A;Accession: S02771
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A;Map position: 5
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Best Local Similarity
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                                                                                                                                                                 QSRQLQDFAALKNRLNNENSDLNRSLEEMDNQLNSLHRLKSTLQSQLDETRRNYDEESRE
                                                                                                                                                                                                                                                                                                                                                                                                                        LQSIVDAGDQSQAAVLQAQQNNSPDNIAATKELIDAA---ETKVNELKQEH----TGLTD 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---INSQLEINKN---SADQIIKDLERQNISYEAVL----TNAGEVIKASSEAGIKLGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSQLEASTSTSTYTRVAAKDYDEAKSNFDTAKSGLENAKTLAEYETKMADLMAALQDMER 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQIASNSETKESTKASEASPSASSSVSSW-SFLSSAKNAL---ISLRDAILNKNSSPTDS
QVAFAAAKVGGGSAGTAGTVQMNVKQLYKTAFSSTSSSSYAAALSDGYSAYKTLNSLYSE
                                                        RQALAATAKNLEHENTILREHLDEEAESKADLTRQISKLNAEIQQWKARFDSEGL-NKLE 1420
                                                                                                        ----PATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIKDALAQALKQPSADGLATAMG
                                                                                                                                                                                                                       GSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAI--ALQGFRSMIEQFNVNN-----
                                                                                                                                                                                                                                                                             QLETLQKLKAKSEAEKSKLQRDLEESQHATDSEVRSRQDLEKALKTIEVQYSELQTKADE 1301
                                                                                                                                                                                                                                                                                                                          ----SPLVKKAEEQISQAQKDIQE------
                                                                                                                                                                                                                                                                                                                                                                                         TERLEQQGG-ATAAQLEANKKREAEIAKLRREKEEDSLNHETAISSLRKRHGDSVAELTE 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHHTNAKLAENNSIIAKLQRLIKELTARNAELEEELEAERNSRQKSDRSRSEAERELEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKQSRDHNIRSLQDEMANQDEAVAKLNKEKKHQEESNRKLNEDLQSEEDKVNHLEKIRNK 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNQLKA-TLESKLSDITGQLEDMQERNEDLARQKKKTDQELSDTKKHVQDLELSLRKAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%; Score 200; DB 1; 18.9%; Pred. No. 0.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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RESULT 37

c97038

phage-related protein, Yqbo B. subtilis homolog [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C97038

R;Nolling, J.; Barcton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
  ;Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Accession: C97038
A;Status: preliminary
A;Accession: C97038
A;Status: preliminary
A;Residues: 1-2052 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79094.1; PID:g15024039; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
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                                     TKQLYSKIQQGISSFKNTVVMSYAQMQMAEQKNYSKLGAEYQQYTKLQRQISKNKGSSKE 1168
                                                                                                                                                                                                                                                                                                                                            WGNSLGDTGKLKDFQSELNKVNKVISETQKNLDTTGYSYDKTTGKIKLLSEASEQIANNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAQKSATLSTMGLNLALGGIVGALTIGLSMAISDIIEKHEEQKQKVDKLKQGYE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLEASTSTSTV-----TRVAAKD----YDEAKSNFDTAKSGLENAKTLA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNALISLRDAILNKNSSPTDSLS
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 LATAMGQVAFAAA----KVGGGSAGT----
                                                                       NNPATAKELQAMEA -- QLTAMS-DQLVGAD- -- - GELPAEIQAIKDALAQALK-QPSADG
                                                                                                                                                   GPSGSAASAGSAAGALKSSNNSGRISLLLDD-----VDNEMAAIALQGFRSMIEQFNV
                                                                                                                                                                                         STDKNGDTIIKNASALQKDTEAFIKGNAVVKDAILNDKELQQAQEKINK------
                                                                                                                                                                                                                             ATKELIDAAETKVNEL-KQEHTGLTDSPLVKKA---EEQISQAQKDIQEIKPSGSDIPIV 336
                                                                                                                                                                                                                                                                   SIEGVARDLTENSDKAKTSIGQLIQSYVTLYKQSDKTALESQKQKGLAQQLALVFGDLTL
                                                                                                                                                                                                                                                                                                       AVLTNAGEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNS-----PDNIA
                                                                                                                                                                                                                                                                                                                                                                                ---SLTEVLKTTDSADQIPAINSQLEINKNSAD------QIIKDLERQNISYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYETKMADLMAALQDMERLANSDPSNNHTEEVNNIKKALEAQKDTIDKLNKLVTLQNQNK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKAKVAAGTMTEE--EASEALEAMQIKM-----KATTVSAEEA----SSANNALS
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                                                                                                                                                                                                                                                                                                                                                                                                                        -----DLTKAMKDNSITADNDDYKNLEKEQSTLENALKRKAELEGKINSVNKSKKNDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 136;
                                                                                                                 · AIQSTTNSYKSYLSYSNQIERNNKLDAQSVADIKKNHQELVPYLNN
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18.8%; Pred.
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AGTVQMNV-
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RESULT 38
S45781
                                                                                    C;Superfamily: yeast probable calcium-binding protein YBL047c;
C;Keywords: calcium binding; EF hand; transmembrane protein
F;167-199/Domain: calmodulin repeat homology <EF1>
                                                                                                                                                                                                                                                                                                                                               Yeast 9, 1355-1371, 1993
A; Title: Sequencing and functional analysis of a 32 560
A; Reference number: S39824; MUID:94205266; PMID:8154187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain S288C
R;Dubols, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy,
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NA-binding protein.
A; Reference number: S50284;
A; Accession: S50284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Apr-2002
C;Accession: S45781; S50284; S45782; S39841; S37339; S42498
R;Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; Submitted to the Protein Sequence Database, August 1994
A;Reference number: S45745
A;Recession: S45781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 579-1381 <SCH>
A;Cross-references: EMBL:Z23261; NID:g313733;
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain S28 R; Scherens, B.; el Bakkoury, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 579-1381 <DUB>
A;Cross-references: EMBL:Z35808; GSPDB:GN00002; MIPS:YBL047c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-961 <DEF>
A; Cross-references: EMBL: X78214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast 10, 1489-1495, 1994 A;Title: The sequence of a 22.4 kb DNA fragment from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-961 <GOF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable calcium-binding protein YBL047c · yeast (Saccharomyces N;Alternate names: hypothetical protein YBL0520
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                                                                                                                                                                                                                    C; Genetics:
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A;Experimental source: strain S288C
                                                                  F;560-576/Domain:
                                                                                                                                                      A; Map position:
                                                                                                                                                                                                  A;Gene:
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                                                                                                                                                                                                  SGD:EDE1; MIPS:YBL047c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAFIQQVL 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTSKAQKNAKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QEEIMOKLTASISKAPOFGYPAVONSADSLOKFAAQLEREFVDGERSLAESOENAFRKO 640
                                                                  transmembrane
                                                                                                                                                                             SGD:S0000143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RIKALQEEIDSLKEASKEIDKLFEQAQSAADSSMNTVDSDNIGDY
  6.2%;
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                                                                  #status predicted
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  Score
Pred.
199.5; DE
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                                                                                                                                                                                                                                                                 PIDN:CAA80797.1;
                      ВВ
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                      Length 1381;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Messenguy,
                                                                                                                                                                                                                                                                 PID: 9313748
                                                                                                                                    calmodulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skala, J.; Goffeau,
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Best Local Similarity

of.

Matches

136;

Conservative

102;

Mismatches

263;

Indels

165;

25;

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A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1957 <CON>
A; Cross-references: EMBL:Z70690; PIDN:CAA94624.1; G: A; Cross-references: EMBL:Z70690; PIDN:CAA94624.1; G: A; Cosmettal source: strain 972h-; cosmid clf3 C; Genetics: A; Gene: SPDB:SPAC1F3.06c
A; Map position: 1
                                                                                                                                                                                                                                                                          hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38077
                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                          R; Connor, R.; Churcher, C.M.; submitted to the EMBL Data Lil
                                                                                                                                                                                                      A; Reference number: Z21767
A; Accession: T38077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKSNFDTAKSGLENAKTLAEYETKMADLMAALQDMERLAN--SDPSNNHTEEVNNIKKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASP----SASSSVSSWSFLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPRSQSLTSSVANNAPQS-VRDDVELPET---LEERDTINNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTERTESDVFDRDVPTLGSQSDSENANTNNGTQSG-NETANPNLTETLSDRFDGDLNEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAYKTLNSLY------SESRSGVQSAISQTANPALSRSVS------RSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QENLYHQHVSK-LQEMFDDLSQRKASFEKADQELKER----NIEYANNVRELSERQMNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKPSGSDIPIVGPSGSAASAGSAAGALKSSNNSGRISLLLDDVDNEMAAIALQGFRSMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYDVNSKQLELNQVTVANLQKEIDGLGEKISVYLTKQKELNDYQKTVEEQHAQLQAKYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EANYHAAESKLNELTTDLQESQTKNAELKEQITNL--NSMTASLQSQLNEKQQQVKQERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFKNQDLFADG-EASAQLSNATTEMANLSNQVNSLSKQASITNDKKSRATQE---LKRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKNALISLRDAILNKNSSPTDSLSQLEASTSTSTVTRVA-----
 144;
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                   Similarity
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   Conservative
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                 6.2%;
                                                                                                                                                                                                                                     M.; Barrell, B.G.; Rajandream,
Library, April 1996
   132;
 Score 199.5; D
Pred. No. 0.86;
2; Mismatches
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                                   DB
   279;
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                                                                                                                                      GSPDB:GN00066; SPDB:SPAC1F3.06c
                                 2
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                                 Length 1957;
   Indels
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   201;
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   28;
                                                                                                                                                   A;Cross-references:
C;Genetics:
                                                                                 A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-2253 <MER>
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                                     A; Gene:
                                                                                                                                   A; Accession: T30336
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   Match
                                     NuMA
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                                                                                   1437 CAEKEQQICSLOQNLKSN
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                                                                                                                                                                                                                                                                                                                                                                                                         475 YKTAFSSTSSSSYA------AALSDGYS-----AYKTLNSLYSE---- 507
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                                                                                                                                615 AAQLEREFVDGERSLAESQENAFRKQPAFIQQVLVNIASLFSGY 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          832 HMQEQTEELKKTHSDVYQQLEGE--RSKVLMIEAKASETKSSQLEKINQLEGELSAANAC 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 ISLRDAILNKNSSPTDSLSQLEASTSTSTYTRVAAKDYDEAKSNFDTAKSGLEN-----A 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 HMESGPESVSSNQSSMNPIINGQIASNSETKESTKASEASPSASSSVSSWSFLSSAKNAL 66
                                                                                                                                                                                                                                                                                                             SRSGVQSAISQTANPALSRSVSRSG------IESQGRSADASQRAAETIVRDSQ 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EQFNV-----NNPATAKELQAMEAQLTAMSDQLVGADG--------
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                                                                                                                                                                                                                                                                     SKYTTNEEVSVDFEQRLLKETSKSAKLEEKMQKLHMELEASFKELLEKNCAIDCLTTEAQ 1396
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                                                                                       -QSLLEEFASLKHSY 1468
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